

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 13, 2003, 14:00:14 : Search time 35 Seconds
(without alignments)
167.515 Million cell updates/sec

Title: SEQ1-EDITED
Perfect score: 199
Sequence: 1 ANSFLXLRHSLKXRCIX.....XXAKXIFZVDVDTLAFWSKH 44

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_101002.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	181	91.0	419	22	AAE08627
2	181	91.0	419	22	AAE08628
3	181	91.0	419	22	AAE08629
4	181	91.0	419	22	AAE08627
5	181	91.0	419	22	AAE08627
6	175	87.9	44	20	AAV18297
7	173	86.9	44	20	AAV18300
8	173	86.9	44	20	AAV18301
9	173	86.9	419	22	AAE08630
10	173	86.9	419	22	AAE08630

11	173	86.9	419	22	AAE08628	Human protein C de
12	169	84.9	44	20	AAV18303	Human protein C GL
13	169	84.9	44	22	AAE08627	Human protein C ga
14	169	84.9	45	19	AAV18300	Human protein C de
15	169	84.9	419	21	AAV18303	Human protein C de
16	169	84.9	419	14	AAV18300	Human protein C de
17	169	84.9	419	14	AAV18300	Human protein C de
18	169	84.9	419	22	AAE08625	Human protein C de
19	169	84.9	419	22	AAE08625	Human protein C de
20	169	84.9	419	22	AAE08625	Human protein C de
21	169	84.9	419	22	AAE08625	Human protein C de
22	169	84.9	419	22	AAE08625	Human protein C de
23	169	84.9	419	22	AAE08625	Human protein C de
24	169	84.9	419	23	AAU98002	Human protein C de
25	169	84.9	419	23	AAU98003	Human protein C de
26	169	84.9	419	23	AAU98004	Human protein C de
27	169	84.9	419	23	AAU98005	Human protein C de
28	169	84.9	419	23	AAU98006	Human protein C de
29	169	84.9	419	23	AAU98007	Human protein C de
30	169	84.9	419	23	AAU98008	Human protein C de
31	169	84.9	419	23	AAU98009	Human protein C de
32	169	84.9	419	23	AAU98010	Human protein C de
33	169	84.9	419	23	AAU98011	Human protein C de
34	169	84.9	419	23	AAU98012	Human protein C de
35	169	84.9	419	23	AAU98013	Human protein C de
36	169	84.9	419	23	AAU98014	Human protein C de
37	169	84.9	419	23	AAU98015	Human protein C de
38	169	84.9	419	23	AAU98016	Human protein C de
39	169	84.9	419	23	AAU98017	Human protein C de
40	169	84.9	419	23	AAU98018	Human protein C de
41	169	84.9	419	23	AAU98019	Human protein C de
42	169	84.9	419	23	AAU98020	Human protein C de
43	169	84.9	419	23	AAU98021	Human protein C de
44	169	84.9	419	23	AAU98022	Human protein C de
45	169	84.9	419	23	AAU98023	Human protein C de

ALIGNMENTS

RESULT 1	AAE08627	standard; Protein: 419 AA.
ID	AAE08627	standard; Protein: 419 AA.
AC	AAE08627	
DT	01-NOV-2001	(first entry)
DE	Human protein C derivative #1.	
XX	Human, protein C derivative; antithrombotic activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassemia.	
XX	Homo sapiens.	
OS	WO200159084-A1.	
PN	16-AUG-2001.	
PD	02-FEB-2001; 2001WO-US01221.	
PF	11-FEB-2000; 2000US-0181948.	
PR	14-MAR-2000; 2000US-0189199.	
XX	(ELIL) LILLY & CO ELI.	
PA	Gerlitz BE, Grinnell BW, Jones BE;	
PI		
XX		

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DR WP1: 2001-514662/56.
DR N-PSDB: AAD15225.
XX Protein C derivative for treating acute coronary syndromes, vascular
XX occlusive disorders, thrombotic disorders and sepsis, comprises
XX substitutions at specified amino acid positions
PS Claim 3; Page 46-47; 59pp; English.
XX
XX The invention relates to human protein C derivatives and nucleic acid
XX molecules encoding such derivatives. These derivatives have increased
XX anticoagulation activity, resistance to serpin inactivation and
XX increased sensitivity to thrombin activation compared to wild type
XX protein C, and retains the biological activity of the wild type human
XX protein C. Protein C derivatives are useful in the manufacture of a
XX medication for the treatment of acute coronary syndromes e.g. myocardial
XX infarction and unstable angina; and disease states predisposing to
XX thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
XX disseminated intravascular coagulation (DIC), burns, transplantations,
XX thalassaemia, sickle cell disease, viral haemorrhagic fever and
XX haemolytic uremic syndrome; sepsis in combination with bacterial
XX permeability increasing protein; thrombotic disorders in combination
XX with an anti-platelet agent; protein C deficiency; acute arterial
XX thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral
XX or peripheral arteries or in vascular grafts in combination with a
XX thrombolytic agent. Nucleic acid molecules of the invention are useful
XX for treating humans with genetically predisposed prothrombotic disorders
XX by gene therapy. The present sequence is human protein C derivative.
XX
SQ Sequence 419 AA;
Query Match 91.0%; Score 181; DB 22; Length 419;
Best Local Similarity 77.3%; Pred. No. 1.1e-21;
Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0.
OY 1 ANSFLXLRHGSILRXCIIXICDFXXAKXIFEDVDVDTLAFWSKH 44
||||| ||||| || |||| || ||||| |||||
Db 1 ANSFLLELRHGSLEKRCIEICDFEAKKIFEDVDVDTLAFWSKH 44

RESULT 2
AAE08628
ID AAE08628 standard; Protein; 419 AA.
XX
XX AAE08628;
XX
XX 01-NOV-2001 (first entry)
XX
XX Human protein C derivative #2.
XX
XX Human; protein C derivative; anticoagulation activity; thrombosis;
XX serpin inactivation; acute coronary syndrome; myocardial infarction;
XX vascular occlusive disorder; hypercoagulable state; angina; sepsis;
XX disseminated intravascular coagulation; DIC; burn; transplantation;
XX sickle cell disease; viral haemorrhagic fever; protein C deficiency;
XX haemolytic uremic syndrome; acute arterial thrombotic occlusion;
XX thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
XX
XX Homo sapiens.
XX
XX WO200159084-A1.
XX
XX 16-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US01221.
XX
XX 11-FEB-2000; 2000US-0181948.
XX
XX 14-MAR-2000; 2000US-0189199.
XX
XX (ELIT ) LILLY & CO ELI.
XX
XX Gerlitz BE, Grinnell BW, Jones BE.
XX

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DR	WP1: 2001-514662/56.
NR	N-PSDB; AAD15226.
XX	Protein C derivative for treating acute coronary syndromes, vascular
PT	occlusive disorders, thrombotic disorders and sepsis, comprises
PT	substitutions at specified amino acid positions
XX	
PS	Claim 4; Page 47-48; 59pp; English.
XX	
CC	The invention relates to human protein C derivatives and nucleic acid
CC	molecules encoding such derivatives. These derivatives have increased
CC	anticoagulation activity, resistance to serpin inactivation and
CC	increased sensitivity to thrombin activation compared to wild type
CC	protein C, and retains the biological activity of the wild type human
CC	protein C. Protein C derivatives are useful in the manufacture of a
CC	medicament for the treatment of acute coronary syndromes e.g. myocardial
CC	infarction and unstable angina; and disease states predisposing to
CC	thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
CC	dissminated intravascular coagulation (DIC), burns, transplantations,
CC	thalassaemia, sickle cell disease, viral haemorrhagic fever and
CC	haemolytic uremic syndrome; sepsis in combination with bacterial
CC	permeability increasing protein; thrombotic disorders in combination
CC	with an anti-platelet agent; protein C deficiency; acute arterial
CC	thrombotic occlusion; thromboembolism or stenosis in coronary, cerebral
CC	or peripheral arteries or in vascular grafts in combination with a
CC	thrombolytic agent. Nucleic acid molecules of the invention are useful
CC	for treating humans with genetically predisposed prothrombotic disorders
CC	by gene therapy. The present sequence is human protein C derivative.
CC	
XX	
SQ	Sequence 419 AA:
	Query Match 91.0%; Score 181; DB 22; Length 419;
	Best Local Similarity 77.3%; Pred. No. 1.le-21;
	Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0.
OY	1 ANSFLXLRHGSILRXXCIXXICDFXAXXIIFZVDVDTLAFWSKH 44 : 1 ANSFLEELRHGSLERECIEICDFFEARKEIFEVDVDTLAFWSKH 44
Db	
RESULT 3	
AAE08629	
ID	AAE08629 standard; Protein; 419 AA.
XX	
AC	AAE08629;
XX	
DT	01-NOV-2001 (first entry)
XX	
DE	Human protein C derivative #3.
XX	
KW	Human; protein C derivative; anticoagulation activity; thrombosis;
KW	serpin inactivation; acute coronary syndrome; myocardial infarction;
KW	vascular occlusive disorder; hypercoagulable state; angina; sepsis;
KW	dissminated intravascular coagulation; DIC; burn; transplantation;
KW	sickle cell disease; viral haemorrhagic fever; protein C deficiency;
KW	haemolytic uremic syndrome; acute arterial thrombotic occlusion;
KW	thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 10
FT	/note= "Encoded by CA"
XX	
PN	W0200159084-A1.
XX	
PD	16-AUG-2001.
XX	
PF	02-FEB-2001; 2001MO-US01221.
XX	
PR	11-FEB-2000; 2000US-0181948.
XX	
PR	14-MAR-2000; 2000US-0189199.
XX	

PA (ELIL) LILLY & CO ELI.
 XX Gerlitz BE, Grinnell BW, Jones BE.
 XX WPI, 2001-514662/56.
 DR N-PSDB; AAD15227.
 XX
 PT Protein C derivative for treating acute coronary syndromes, vascular
 PT occlusive disorders, thrombotic disorders and sepsis, comprises
 PT substitutions at specified amino acid positions
 XX
 XX Claim 5: Page 48-49; 59pp: English.
 PS
 XX The invention relates to human protein C derivatives and nucleic acid
 CC molecules encoding such derivatives. These derivatives have increased
 CC anticoagulation activity, resistance to serpin inactivation and
 CC increased sensitivity to thrombin activation compared to wild type
 CC protein C, and retains the biological activity of the wild type human
 CC protein C. Protein C derivatives are useful in the manufacture of a
 CC medicament for the treatment of acute coronary syndromes e.g. myocardial
 CC infarction and unstable angina; and disease states predisposing to
 CC thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
 CC disseminated intravascular coagulation (DIC), burns, transplantations,
 CC cholesteraemia, sickle cell disease, viral haemorrhagic fever and
 CC haemolytic uremic syndrome; sepsis in combination with bacterial
 CC permeability increasing protein; thrombotic disorders in combination
 CC with an anti-platelet agent; protein C deficiency; acute arterial
 CC thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral
 CC or peripheral arteries or in vascular grafts in combination with a
 CC thrombolytic agent. Nucleic acid molecules of the invention are useful
 CC for treating humans with genetically predisposed prothrombotic disorders
 CC by gene therapy. The present sequence is human protein C derivative.
 XX
 SO Sequence 419 AA:

Query Match 91.0%; Score 181; DB 22; Length 419;
 Best Local Similarity 77.3%; Pred. No. 1.1e-21;
 Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 ANSEFLXXLRHGSLRXICIXXICDPPXAXKXFFZVDOTLAFMSKH 44
 1 ANSFLELRHGSLRECTERICDPEEKELFEVDOTLAFMSKH 44

RESULT 4
 AAB82675
 ID AAB82675 standard; Protein; 419 AA.
 AC AAB82675;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE Human protein C derivative (S11G/Q32E/N33D/L194S).
 XX
 KW Protein C; human; coronary syndrome; thrombosis; angina;
 KW myocardial infarction; vascular occlusive disorder;
 KW hypercoagulation; sepsis; protein C deficiency; occlusion;
 KW thromboembolism; stenosis; antibacterial; immunosuppressive;
 KW thrombolytic; cardiac; antiangiinal; anticoagulant; therapy;
 KW mutant; mutain.
 XX
 OS Homo saplens.
 OS Synthetic.
 FH
 XX Key Location/Qualifiers
 FT MISC-difference 11 /note= "Ser in wild-type protein"
 FT MISC-difference 32 /note= "Gln in wild-type protein"
 FT MISC-difference 33 /note= "Gln in wild-type protein"
 FT MISC-difference 194 /note= "Asn in wild-type protein"
 FT MISC-difference 194 /note= "Leu in wild-type protein"

FT Domain 1..45
 FT /note= "Gla. domain"
 FT Disulfide-bond 50..69
 FT Disulfide-bond 59..64
 FT Disulfide-bond 80..89
 FT Disulfide-bond 98..109
 FT Disulfide-bond 120..133
 FT Disulfide-bond 141..277
 FT Disulfide-bond 146..212
 FT Disulfide-bond 331..345
 FT Disulfide-bond 356..384
 FT Disulfide-bond 156..157
 FT /note= "Cleaveage makes a 2-chain inactive
 FT precursor (155-amino acid light chain
 FT attached via a disulfide bond to a
 FT 262-amino acid heavy chain)"
 FT Modified-site 6
 FT /note= "gamma-carboxylated"
 FT Modified-site 7
 FT /note= "gamma-carboxylated"
 FT Modified-site 14
 FT /note= "gamma-carboxylated"
 FT Modified-site 16
 FT /note= "gamma-carboxylated"
 FT Modified-site 19
 FT /note= "gamma-carboxylated"
 FT Modified-site 20
 FT /note= "gamma-carboxylated"
 FT Modified-site 25
 FT /note= "gamma-carboxylated"
 FT Modified-site 26
 FT /note= "gamma-carboxylated"
 FT Modified-site 158..169
 FT /note= "gamma-carboxylated"
 FT Peptide
 FT /note= "activation peptide; removal activates the
 FT 2-chain zymogen"
 FT Cleavage-site 169..170
 FT /note= "chrombin cleavage site"
 FT Modified-site 29
 FT /note= "N-glycosylated"
 FT Modified-site 248
 FT /note= "N-glycosylated"
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 FT Modified-site
 FT /note= "N-glycosylated"
 XX WO200157193-A2.
 PN
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 PD 09-AUG-2001.
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 PD 19-JAN-2001: 2001WO-US00020.
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 XX 02-FEB-2000: 2000US-0179801.
 PR 14-MAR-2000: 2000US-0189197.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PT Gerlitz BE, Jones BE.
 XX
 DR WPI; 2001-496919/54.
 DR N-PSDB; AAB26363.
 XX
 PT Novel human protein C derivative for treating, e.g., myocardial
 PT infarction, unstable angina, sepsis, thrombotic disorders, acute
 PT arterial thrombotic occlusion, and thromboembolism -
 XX
 PS Claim 3: Page 52-53; 63pp: English.
 CC The present sequence is that of a claimed human protein C
 CC derivative in which Ser at amino acid position 11 of the mature
 CC wild-type protein C sequence (see AAB82673) is substituted with
 CC Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and
 CC Leu at position 194 with Ser. The protein is an example of protein

C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).

SQ Sequence 419 AA;

Query Match	91.0%;	Score 181;	DB 22;	Length 419;
Best Local Similarity	77.3%;	Pred. No. 1.1e-21;		
Matches 34;	Conservative 1;	Mismatches 9;	Indels 0;	Gaps 0;

Q7

1 ANSFLXXLHRGSLARRCIXXICDFEAXAKIYFDVDDDTLAFWSKH 44
||||| ||||| | |||| | : : ||||| |||||
||||| ||||| | |||| | : : ||||| |||||

D6

1 ANSFLEELRHGSLERECIEEICDFEEAKEIFEEDVDTLTAFWSKH 44

RESULT 5
AAB82676

AC AAB82676;

DT 15-OCT-2001 (first entry)

Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).

KM Protein C; human; coronary syndrome; thrombosis; angina;
KM myocardial infarction; vascular occlusive disorder;
KM hypercoagulation; sepsis; protein C deficiency; occlusion;
KM thromboembolism; stenosis; antibacterial; immunosuppressive;
KM thrombolytic; cadiant; antiangiinal; anticoagulant; therapy
KM mutant; mutcin.

05 Homo sapiens.
05 Synthetic.

FH	Key	Location/Qualifiers
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99	99	99
100	100	100

/note= "Ser in wild-type protein"

/note= "Gln in wild-type protein"

/note= "Asn in wild-type protein"

/note= "Leu in wild-type protein"

	FT	FT
/note= "Thr in wild-type protein"		

FT	/note= "Gla domain"
FT	

Disulfide-bond


FT Disulfide-bond

Disulfide-bond

Disulfide-bond

FT Cleavage-site

3



```
/note= "cleavage makes a 2-chain inactive
```

FT precursor (155-amino acid light chain
FT attached via a disulfide bond to a
FT 262-amino acid heavy chain)"

CC Thrombotic occlusion, thromboembolism, or stenosis in coronary,
 CC cerebral or peripheral arteries or in vascular grafts. Human
 CC patients with genetically predisposed prothrombotic disorders may
 CC be treated by gene therapy (all claimed).
 XX

SO Sequence 419 AA:

Query Match 91.0%; Score 181; DB 22; Length 419;
 Best Local Similarity 77.3%; Pred. No. 1.1e-21;
 Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXXICDPFXAKXIFZDVDDTLAFWSKH 44
 DB 1 ANSFLXELRHGSLRRCIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 6

AAI18297
 ID AAY18297 standard; peptide; 44 AA.

AC AAY18297;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.

KW GLA domain; muteln; vitamin K-dependent protein; clotting disorder;

therapy.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT Misc-difference 1..44 /note="xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"

XX WO9920767-A1.

XX 29-APR-1999.

XX 20-OCT-1998; 98WO-US22152.

XX 23-OCT-1997; 97US-0955636.

XX (MINU) UNIV MINNESOTA.

XX Nelstuen GL;

XX WPI: 1999-288309/24.

PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders

XX Claim 6: Page 78; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.

SO Sequence 44 AA:

Query Match 87.9%; Score 175; DB 20; Length 44;

Best Local Similarity 95.5%; Pred. No. 1e-21;
 Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXXICDPFXAKXIFZDVDDTLAFWSKH 44
 XXX

DB 1 ANSFLXXLRHGSIXRCIXXICDPFXAKXIFEDVDDTLAFWSKH 44

RESULT 7

AAI18300
 ID AAY18300 standard; peptide; 44 AA.

AC AAY18300;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.

KW GLA domain; muteln; vitamin K-dependent protein; clotting disorder;

therapy.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT Misc-difference 1..44 /note="xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"

XX WO9920767-A1.

XX 29-APR-1999.

XX 20-OCT-1998; 98WO-US22152.

XX 23-OCT-1997; 97US-0955636.

XX (MINU) UNIV MINNESOTA.

XX Nelstuen GL;

XX WPI: 1999-288309/24.

PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders

XX Claim 9: Page 79; 86pp; English.

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GLA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the
 CC GLA domain results in a protein which has enhanced membrane binding
 CC affinity as compared to the native protein.

SO Sequence 44 AA:

Query Match 86.9%; Score 173; DB 20; Length 44;
 Best Local Similarity 95.5%; Pred. No. 2.1e-21;
 Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXXICDPFXAKXIFZDVDDTLAFWSKH 44
 DB 1 ANSFLXXLRHGSIXRCIXXICDPFXAKXIFEDVDDTLAFWSKH 44

RESULT 8

AAI18301
 ID AAY18301 standard; peptide; 44 AA.

AC AAY18301;

DT 17-AUG-1999 (first entry)

XX Modified GLA domain of vitamin K-dependent protein.

```

KM GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KW therapy.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
XX WO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelstuen GL.
XX
XX WPI, 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Claim 9; Page 82; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX SQ Sequence 44 AA;
XX
XX Query Match 86.9%; Score 173; DB 20; Length 44;
XX Best Local Similarity 95.5%; Pred. No. 2.1e-21;
XX Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX OY 1 ANSFLXXLRHGSIXRCIXXICDFXXAKXIFZDVDDTLAFWSKH 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 ANSFLXXLRHGSIXRCIXXICDFXXAKXIFZDVDDTLAFWSKH 44
XX
XX Db 1 ANSFLXXLRHGSIXRCIXXICDFXXAKXIFZDVDDTLAFWSKH 44
XX
XX RESULT 9
XX AAE08630
XX ID AAE08630 standard; Protein: 419 AA.
XX
XX AAE08630;
XX
XX 01-NOV-2001 (first entry)
XX
XX Human protein C derivative #4.
XX
XX Human; protein C derivative; anticoagulation activity; thrombosis;
XX serpin inactivation; acute coronary syndrome; myocardial infarction;
XX vascular occlusive disorder; hypercoagulable state; angina; sepsis;
XX disseminated intravascular coagulation; DIC; burn; transplantation;
XX sickle cell disease; viral haemorrhagic fever; protein C deficiency;
XX haemolytic uremic syndrome; acute arterial thrombotic occlusion;
XX thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
XX
XX Homo sapiens.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 10
XX /note= "His in wild-type protein"
XX
XX PD 16-AUG-2001.

```

```

XX
XX 02-FEB-2001; 2001WO-US01221.
XX
XX 11-FEB-2000; 2000US-0181948.
XX
XX 14-MAR-2000; 2000US-0189199.
XX
XX (ELIT ) LILLY & CO ELI.
XX
XX Gerlitz BE, Grinnell BW, Jones BE;
XX
XX WPI, 2001-514662/56.
XX
XX N-PSDB; AAD15228.
XX
XX Protein C derivative for treating acute coronary syndromes, vascular
XX occlusive disorders, thrombotic disorders and sepsis, comprises
XX substitutions at specified amino acid positions :
XX
XX Claim 6; Page 50-51; 59pp; English.
XX
XX The invention relates to human protein C derivatives and nucleic acid
XX molecules encoding such derivatives. These derivatives have increased
XX anticoagulation activity, resistance to serpin inactivation and
XX increased sensitivity to thrombin activation compared to wild type
XX protein C, and retains the biological activity of the wild type human
XX protein C. Protein C derivatives are useful in the manufacture of a
XX medicament for the treatment of acute coronary syndromes e.g. myocardial
XX infarction and unstable angina; and disease states predisposing to
XX thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
XX disseminated intravascular coagulation (DIC), burns, transplantations,
XX thalassaemia, sickle cell disease, viral haemorrhagic fever and
XX haemolytic uremic syndrome; sepsis in combination with bacterial
XX permeability increasing protein; thrombotic disorders in combination
XX with an anti-platelet agent; protein C deficiency; acute arterial
XX thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral
XX or peripheral arteries or in vascular grafts in combination with a
XX thrombolytic agent. Nucleic acid molecules of the invention are useful
XX for treating humans with genetically predisposed prothrombotic disorders
XX by gene therapy. The present sequence is human protein C derivative.
XX
XX SQ Sequence 419 AA;
XX
XX Query Match 86.9%; Score 173; DB 22; Length 419;
XX Best Local Similarity 75.0%; Pred. No. 2.3e-20;
XX Matches 33; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
XX
XX OY 1 ANSFLXXLRHGSIXRCIXXICDFXXAKXIFZDVDDTLAFWSKH 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 ANSFLXELRGSLRRCIEICDFEAKEIFZDVDDTLAFWSKH 44
XX
XX Db 1 ANSFLXELRGSLRRCIEICDFEAKEIFZDVDDTLAFWSKH 44
XX
XX RESULT 10
XX AAB82677
XX ID AAB82677 standard; Protein: 419 AA.
XX
XX AAB82677;
XX
XX 15-OCT-2001 (first entry)
XX
XX Human protein C derivative (H10Q/S11G/O32E/M33D/L194S).
XX
XX Protein C; human; coronary syndrome; thrombosis; angina;
XX myocardial infarction; vascular occlusive disorder;
XX hypercoagulable state; sepsis; protein C deficiency; occlusion;
XX thromboembolism; stenosis; antibacterial; immunosuppressive;
XX thrombolytic; cardiant; antianginal; anticoagulant; therapy;
XX mutant; mutein.
XX
XX Homo sapiens.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 10
XX /note= "His in wild-type protein"
XX
XX FT

```

```

FT Misc-difference 11 /note= "Ser in wild-type protein"
FT Misc-difference 32 /note= "Gln in wild-type protein"
FT Misc-difference 33 /note= "Asn in wild-type protein"
FT Misc-difference 194 /note= "Leu in wild-type protein"
FT Domain 1..45 /note= "Gla domain"
FT Disulfide-bond 50..69
FT Disulfide-bond 59..64
FT Disulfide-bond 80..89
FT Disulfide-bond 98..109
FT Disulfide-bond 120..133
FT Disulfide-bond 141..277
FT Disulfide-bond 196..212
FT Disulfide-bond 331..345
FT Disulfide-bond 356..384
FT Cleavage-site 156..157 /note= "cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
FT Modified-site 6 /note= "gamma-carboxylated"
FT Modified-site 7 /note= "gamma-carboxylated"
FT Modified-site 14 /note= "gamma-carboxylated"
FT Modified-site 16 /note= "gamma-carboxylated"
FT Modified-site 19 /note= "gamma-carboxylated"
FT Modified-site 20 /note= "gamma-carboxylated"
FT Modified-site 25 /note= "gamma-carboxylated"
FT Modified-site 26 /note= "gamma-carboxylated"
FT Modified-site /note= "gamma-carboxylated"
FT Peptide 158..169 /note= "activation peptide; removal activates the 2-chain zymogen"
FT Cleavage-site 169..170 /note= "thrombin cleavage site"
FT Modified-site 29 /note= "N-glycosylated"
FT Modified-site 248 /note= "N-glycosylated"
FT Modified-site 313 /note= "N-glycosylated"
FT Modified-site 329 /note= "N-glycosylated"
FT Modified-site /note= "N-glycosylated"
XX WO200157193-A2.
XX
XX 09-AUG-2001.
XX
XX 19-JAN-2001: 2001WO-US00020.
XX
XX 02-FEB-2000: 2000US-0179801.
XX
XX 14-MAR-2000: 2000US-0189197.
XX
XX (ELIT ) LILLY & CO ELI.
XX
XX Gerlitz BE, Jones BE;
XX
XX WPI: 2001-496919/54.
XX
XX N-PSDB: AAH26365.
XX
XX Novel human protein C derivative for treating, e.g., myocardial
XX infarction, unstable angina, sepsis, thrombotic disorders, acute
XX arterial thrombotic occlusion, and thromboembolism -

```

```

XX Claim 5; Page 54-55; 63pp; English.
PS
XX The present sequence is that of a claimed human protein C derivative
CC in which His at position 10 of the mature wild-type protein C
CC sequence (see AAB82673) is substituted with Gln, Ser at position 11
CC with Gly, Gln at position 32 with Gln, Asn at position 33 with Asp,
CC and Leu at position 194 with Ser. It is an example of protein C
CC derivatives of the invention that have at least 2 amino acid
CC substitutions, but which have increased anticoagulant activity and
CC resistance to inactivation by serpins compared with the wild-type
CC protein. A method of producing the derivatives using recombinant
CC DNA methods is claimed. The protein C derivatives are useful for
CC treating coronary syndromes and disease states predisposing to
CC thrombosis (e.g. myocardial infarction and unstable angina),
CC vascular occlusive disorders and hypercoagulable states, sepsis (in
CC combination with bactericidal permeability increasing protein or
CC with tissue factor pathway inhibitor), thrombotic disorders (in
CC combination with an anti-platelet agent or by local delivery through
CC an intracoronary catheter), protein C deficiency, acute arterial
CC thrombotic occlusion, thromboembolism, or stenosis in coronary,
CC cerebral or peripheral arteries or in vascular grafts. Human
CC patients with genetically predisposed prothrombotic disorders may
CC be treated by gene therapy (all claimed).
XX
SQ Sequence 419 AA:
XX
XX Query Match 86.9%; Score 173; DB 22; Length 419;
XX Best Local Similarity 75.0%; Pred. No. 2,3e-20;
XX Matches 33; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
XX
OY 1 ANSEFLXXLRHGSIXRXICIXXICDFXXAKKIFZDVDDTLAFMSKH 44
DB 1 ANSFLELRGSLERDCIEICDFEAKKIFEDVDTLAFMSKH 44
XX
RESULT 11
AAB82678
ID AAB82678 standard; Protein; 419 AA.
XX
XX AAB82678;
XX
XX 15-OCT-2001 (first entry)
XX
XX Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S).
XX
XX Protein C; human; coronary syndrome; thrombosis; angina;
XX myocardial infarction; vascular occlusive disorder;
XX hypercoagulation; sepsis; protein C deficiency; occlusion;
XX thromboembolism; stenosis; antibacterial; immunosuppressive;
XX thrombolytic; cardiac; antiangiinal; anticoagulant; therapy;
XX mutant; mutlein.
XX
XX Homo sapiens.
XX Synthetic.
OS
XX
XX key Location/Qualifiers
FT Misc-difference 10 /note= "His in wild-type protein"
FT Misc-difference 11 /note= "Ser in wild-type protein"
FT Misc-difference 32 /note= "Gln in wild-type protein"
FT Misc-difference 33 /note= "Gln in wild-type protein"
FT Misc-difference 33 /note= "Asn in wild-type protein"
FT Misc-difference 194 /note= "Leu in wild-type protein"
FT Misc-difference 254 /note= "Thr in wild-type protein"
FT Domain 1..45 /note= "Gla domain"
FT Disulfide-bond 50..69

```

FT Disulfide-bond 59..64
 FT Disulfide-bond 80..89
 FT Disulfide-bond 98..109
 FT Disulfide-bond 120..133
 FT Disulfide-bond 141..177
 FT Disulfide-bond 156..212
 FT Disulfide-bond 331..345
 FT Disulfide-bond 356..384
 FT Disulfide-bond 156..157
 FT /note="cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
 FT
 FT Modified-site 6
 FT /note="gamma-carboxylated"
 FT Modified-site 7
 FT /note="gamma-carboxylated"
 FT Modified-site 14
 FT /note="gamma-carboxylated"
 FT Modified-site 16
 FT /note="gamma-carboxylated"
 FT Modified-site 19
 FT /note="gamma-carboxylated"
 FT Modified-site 20
 FT /note="gamma-carboxylated"
 FT Modified-site 25
 FT /note="gamma-carboxylated"
 FT Modified-site 26
 FT /note="gamma-carboxylated"
 FT Peptide 158..169
 FT /note="activation peptide; removal activates the 2-chain zymogen"
 FT
 FT Cleavage-site 169..170
 FT /note="thrombin cleavage site"
 FT Modified-site 29
 FT /note="N-glycosylated"
 FT Modified-site 248
 FT /note="N-glycosylated"
 FT Modified-site 313
 FT /note="N-glycosylated"
 FT Modified-site 329
 FT /note="N-glycosylated"
 FT
 FT WO200157193-A2.
 FT
 FT 09-AUG-2001.
 FT
 FT 19-JAN-2001: 2001WO-US00020.
 FT
 FT 02-FEB-2000: 2000US-0179801.
 FT 14-MAR-2000: 2000US-0189197.
 FT
 FT (ELIL) LILLY & CO ELI.
 FT
 FT Gerlitz BE, Jones BE.
 FT
 FT WPI: 2001-496919/54.
 FT
 FT Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism -
 FT
 FT
 FT Claim 6: Page 56-57; 63pp; English.
 FT
 FT The present sequence is that of a claimed human protein C derivative in which His at position 10 of the wild-type protein C sequence (see AAB82673) is substituted with Gln, Ser at position 11 with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, Leu at position 194 with Ser, and Thr at position 254 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type

CC protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g., myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human CC patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).
 CC
 CC Sequence 419 AA:
 CC
 CC Query Match 86.9%; Score 173; DB 22; Length 419;
 CC Best Local Similarity 75.0%; Pred. No. 2.3e-20;
 CC Matches 33; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
 CC
 CC QY 1 ANSFLXLRHGSIXRXCIXXICDPEXXAKXIFZVDVDTLAFWSKH 44.
 CC 1 ANSFLERLRGSLERCEICDPEAKELFEDVDTLAFWSKH 44
 CC
 CC DB
 CC
 CC RESULT 12
 CC AAY18303
 CC ID AAY18303 standard; peptide; 44 AA.
 CC
 CC AAY18303;
 CC
 CC DT 17-AUG-1999 (first entry)
 CC
 CC DE Human protein C GLA domain.
 CC
 CC DX
 CC KW GLA domain; vitamin K-dependent protein; clotting disorder; therapy.
 CC
 CC OS Homo sapiens.
 CC
 CC FH Key Location/Qualifiers
 CC FT Misc-difference 1..44
 CC FT /note="Xaa=gamma-carboxyglutamic acid, or glutamic acid"
 CC FT
 CC PN MO9920767-A1.
 CC
 CC PD 29-APR-1999.
 CC
 CC XX 20-OCT-1998: 98WO-US22152.
 CC PF
 CC XX 23-OCT-1997: 97US-0955636.
 CC PR
 CC XX (MINU) UNIV MINNESOTA.
 CC PA
 CC XX Nelsetuen GL:
 CC PI
 CC DR WPI: 1999-288309/24.
 CC
 CC XX vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
 CC PT
 CC XX
 CC PS Disclosure: Page 14; 86pp; English.
 CC
 CC XX This sequence is the protein C GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
 CC
 CC

SQ Sequence 44 AA: 84.9%; Score 169; DB 20; Length 44;
 Query Match Best Local Similarity 93.2%; Pred. No. 1e-20;
 Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXXICDFXAKXIF2DVEDTLAFWSKH 44
 1 ANSFLXXLRHGSIXRCIXXICDFXAKXIFQNVDDTLAFWSKH 44

DB 1 ANSFLXXLRHGSIXRCIXXICDFXAKXIFQNVDDTLAFWSKH 44

RESULT 13
 AAB36402 standard; peptide: 44 AA.
 AAB36402;
 27-FEB-2001 (first entry)
 Human protein C gamma-carboxyglutamic acid domain SEQ ID NO:1.
 Vitamin K-dependent protein; factor VII; protein C; Gla domain;
 gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 factor X; prothrombin; enhanced membrane binding affinity;
 clot formation; thrombolytic; haemostatic; bleeding disorder;
 thrombosis; clotting disorder; haemophilia A; haemophilia B;
 liver disease.
 Homo sapiens.
 WO200066753-A2.
 09-NOV-2000.
 28-APR-2000: 2000WO-US11416.
 29-APR-1999: 9905-0302239.
 (MINU) UNIV MINNESOTA.
 Nelsstuen GL:
 WPI: 2001-007226/O1.
 Novel vitamin K-dependent polypeptide useful for treating clotting disorders such as thrombosis and hemophilia, comprises modified gamma-carboxy glutamic acid domain that enhances membrane binding affinity -
 Example 5; Page 42; 81pp: English.
 The present invention describes a vitamin K-dependent polypeptide (I) comprising a modified gamma-carboxy glutamic acid (Gla) domain having at least one amino acid substitution, that enhances membrane binding affinity and the activity of the polypeptide relative to a corresponding native vitamin K-dependent polypeptide and inhibits clot formation. (I) can have thrombolytic and haemostatic activities, and can be used as an inhibitor of clot formation. (I) is useful for decreasing clot formation in a mammal, a factor VII or factor IX containing a modified Gla domain is useful for increasing clot formation and for treating a bleeding disorder, including thrombosis and clotting disorders such as haemophilia A, haemophilia B and liver disease. The present sequence represents a human protein C Gla domain sequence, given in the exemplification of the present invention.

Query Match 84.9%; Score 169; DB 22; Length 44;
 Best Local Similarity 93.2%; Pred. No. 1e-20;
 Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXXICDFXAKXIF2DVEDTLAFWSKH 44
 1 ANSFLXXLRHGSIXRCIXXICDFXAKXIF2DVEDTLAFWSKH 44

DB 1 ANSFLXXLRHGSIXRCIXXICDFXAKXIFQNVDDTLAFWSKH 44
 RESULT 14
 AAW75710 standard; protein: 45 AA.
 AAW75710;
 08-DEC-1998 (first entry)
 Partial human protein C amino acid sequence.
 Gamma carboxyglutamic acid; human protein C; Gla domain; chimera;
 pRC/RSV; RSV-PC; amplification, PCR, primer: transfection; anticoagulant;
 human 293 cell; protein S; myocardial infarction; venous thrombosis;
 disseminated intravascular coagulation; thromboembolic disease; lupus;
 adult respiratory distress syndrome; factor V leiden; stroke.
 Homo sapiens.
 Key location/Qualifiers
 FT Misc-difference 6 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 7 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 14 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 16 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 19 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 20 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 25 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 26 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 29 /note= "Gamma carboxyglutamic acid"
 FT Misc-difference 29 /note= "Gamma carboxyglutamic acid"
 W09820118-A1.
 14-MAY-1998.
 07-NOV-1997: 97WO-US20376.
 25-JUL-1997: 97US-0053768.
 08-NOV-1996: 96US-0745254.
 (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 Esmon CT, Smirnov M;
 WPI: 1998-286934/25.
 Protein C chimeric proteins for use as anticoagulants - having gamma carboxyglutamic acid region replaced with vitamin K dependent clotting factor e.g. prothrombin
 Example 1; Page 15; 42pp: English.
 The present sequence represents the first three exons of the human protein C protein, which contains gamma carboxyglutamic acid modified residues. This sequence was replaced with the corresponding regions of modified human prothrombin (AAW75709), to create a protein C prothrombin Gla domain chimera. To produce this chimera, the wild-type protein C cDNA was ligated into pRC/RSV to form RSV-PC, and then was digested with restriction enzymes to remove the first three exons and the first codon of exon four. The prothrombin cDNA was amplified, digested, and then ligated into RSV-PC at the identical site where the protein C cDNA exons 1-3 had been removed. This construct was then transfected into human 293 cells, from which the chimeric protein can be purified. This

CC chimeric protein, can be used as an anticoagulant, to treat disorders where
CC protein S is low, some forms of lupus, following stroke or myocardial
CC infarction, after venous thrombosis and in disseminated intravascular
CC coagulation, adult respiratory distress syndrome, in thromboembolic
CC disease or factor V Leiden.

XX
SQ Sequence 45 AA;

Query Match 84.9%; Score 169; DB 19; Length 45;
Best Local Similarity 93.2%; Pred. No. 1e-20;
Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANSFLXLRHSGSLRXRCIXXICDFXXAKXIFZVDVDTLAFWSKH 44
|||||
DB 1 ANSFLXLRHSGSLRXRCIXXICDFXXAKXIFZVDVDTLAFWSKH 44

RESULT 15

AAV56803
ID AAV56803 standard; Protein; 415 AA.

XX
AC AAV56803;

XX
DT 27-MAR-2000 (first entry)

XX
DE Truncated human protein C polypeptide.

XX
KM Protein C; truncated; thrombotic disorder; vascular disorder; stroke;
KM hypercoagulable state; myocardial infarction; unstable angina; sepsis;
KM adult respiratory distress syndrome; sickle cell anemia; human.

XX
OS Homo sapiens.

XX
PN W09963070-A1.

XX
PD 09-DEC-1999.

XX
PF 01-JUN-1999; 99WO-US11969.

XX
PR 01-JUN-1998; 98US-0087585.

XX
PA (ELIL) LILLY & CO ELI.

XX
PI Huang L, Riggin RM;

XX
PI MPI: 2000-086975/07.

XX
DR N-PSDB: AA246750.

XX
PT Novel polypeptide useful for treating thrombotic and vascular diseases
PT and hypercoagulation, e.g. stroke

XX
PS Claim 2; Page 22-23; 23pp; English.

XX
CC This represents a human protein C polypeptide having a light chain and
CC a truncated heavy chain. The protein can be produced by standard
CC recombinant methodologies. The truncated protein C is used to treat a
CC wide range of thrombotic or vascular disorders or hypercoagulable states,
CC e.g. stroke; myocardial infarction; unstable angina; sepsis; adult
CC respiratory distress syndrome; sickle cell anemia etc. The truncated
CC protein C retains the activity of full-length protein C but does not
CC undergo C-terminal cleavage, of the heavy chain, during activation.

XX
SQ Sequence 415 AA;

Query Match 84.9%; Score 169; DB 21; Length 415;
Best Local Similarity 72.7%; Pred. No. 1.1e-19;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANSFLXLRHSGSLRXRCIXXICDFXXAKXIFZVDVDTLAFWSKH 44
|||||
DB 1 ANSFLXLRHSGSLRXRCIXXICDFXXAKXIFZVDVDTLAFWSKH 44

Search completed: May 13, 2003, 14:03:16
Job time : 36 secs

GenCore version 5.1.4.p5.4578
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OW protein - protein search, using sw model

Run on: May 13, 2003, 14:02:03 ; Search time 18 seconds
(without alignments)
234.995 Million cell updates/sec

Title: SEQ1-EDITED
Perfect score: 199
Sequence: 1 ANSFLXXLRIGSLXRCIXX.....XXAKXIFZVDVDTLAFWSKH 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	84.9	461	1 KXHU	protein C (activat
2	140	70.4	461	1 JY0210	protein C (activat
3	139	69.8	461	1 S18994	protein C (activat
4	122	61.3	456	1 KXBO	protein C (activat
5	112	56.3	482	1 EXRT	coagulation factor
6	108	54.3	492	1 EXBO	coagulation factor
7	107	53.8	488	1 EXHU	coagulation factor
8	101	50.8	443	2 I46932	coagulation factor
9	98	49.2	466	1 KFHU7	coagulation factor
10	84	42.2	407	1 KFB07	coagulation factor
11	83.5	42.0	617	2 S10511	thrombin (EC 3.4.2
12	83.5	42.0	618	2 A35827	thrombin (EC 3.4.2
13	81	40.7	622	1 TBHU	thrombin (EC 3.4.2
14	80	40.2	475	1 EXCH	coagulation factor
15	79	39.7	642	2 S53434	plasma protein S p
16	79	39.7	656	1 KXHU5	plasma protein S p
17	78	39.2	472	1 A30351	coagulation factor
18	78	39.2	459	2 J00419	coagulation factor
19	78	39.2	446	2 S38819	plasma protein S -
20	77	38.7	675	1 KXBOS	plasma protein S p
21	75	37.7	675	1 KXRTS	plasma protein S p
22	74	37.2	461	1 KFHU	coagulation factor
23	72	36.2	416	1 KFB0	plasma protein S p
24	71	35.7	416	1 KFB0	coagulation factor
25	69	34.7	625	1 TBBO	thrombin (EC 3.4.2
26	68	34.2	675	1 KXMS	plasma protein S p
27	66.5	33.4	396	1 KXBOZ	plasma protein Z -
28	62.5	31.4	422	1 KXHUZ	plasma protein Z p
29	59	29.6	673	2 A48089	growth arrest-spec

30	58	29.1	674	2	155476	growth potentiatin
31	57	28.6	678	2	B48089	growth arrest-spec
32	56.5	28.4	594	2	D84859	probable MAP kinas
33	54.5	27.4	603	2	C96575	probable MAP kinas
34	52.5	26.4	576	2	G96763	probable MAP kinas
35	52	26.1	606	2	T40556	hypothetical prote
36	49	24.6	730	2	G64062	primosomal replica
37	49	24.6	1363	2	I58375	protein-tyrosine k
38	49	24.6	1684	2	T02367	hypothetical prote
39	49	24.6	1694	2	A83512	hypothetical prote
40	48.5	24.4	510	2	B82918	ammonium transport
41	48	24.1	558	1	S27994	alcohol dehydrogen
42	48	24.1	1235	2	D32433	V56 expression sit
43	48	24.1	1298	2	A48999	protein-tyrosine k
44	47.5	23.9	323	2	T25948	hypothetical prote
45	47	23.6	182	2	JC1189	tyrosine kinase re

ALIGNMENTS

RESULT 1

KXHU
protein C (activated) (EC 3.4.21.69) precursor - human
N:Alternate names: autoprothrombin IIA; plasma protein C
C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A22331; A25426; A21781; A23789; A00927
R:Foster, D.C.; Yoshitake, S.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
A>Title: The nucleotide sequence of the gene for human protein C.
A:Reference number: A22331; MUID:85270390; PMID:2991887
A:Accession: A22331
A:Molecule type: DNA
A:Residues: 1-461 <POS1>
A:Cross-references: GB:M1228; NID:g190333; PIDN:AAA60166.1; PID:g190334
R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A>Title: Evolution and organization of the human protein C gene.
A:Reference number: A25426; MUID:86120978; PMID:3511471
A:Accession: A25426
A:Molecule type: DNA
A:Residues: 1-445, 446-461 <PLU>
A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
R:Foster, D.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A>Title: Characterization of a cDNA coding for human protein C.
A:Reference number: A21781; MUID:84272714; PMID:6589623
A:Accession: A21781
A:Molecule type: mRNA
A:Residues: 107-107-461 <POS2>
A:Cross-references: GB:X02055; NID:g190332; PIDN:AAA60164.1; PID:g190333
R:Beckman, R.J.; Schmidt, R.J.; Santetere, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.
Nucleic Acids Res. 13, 5233-5247, 1985
A>Title: The structure and evolution of a 461 amino acid human protein C precursor an
A:Reference number: A23789; MUID:85269639; PMID:2991859
A:Accession: A23789
A:Molecule type: mRNA
A:Residues: 1-461 <BEC>
A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
R:Milletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 265, 11397-11404, 1990
A>Title: Beta protein C is not glycosylated at asparagine 329. The rate of translatio
A:Reference number: A4605; MUID:90293094; PMID:1694179
A:Contents: annotation; carbohydrate binding sites; activation peptide
A>Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is
J.Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A>Title: O-linked fucose is present in the first epidermal growth factor domain of f
A:Reference number: A4606; MUID:92184750; PMID:1544894
A:Contents: annotation; beta-hydroxyaspartic acid
A:Comment: protein C is the zymogen of the vitamin K-dependent serine proteinase that
ivation of factor Va is strongly enhanced by complexing with protein S. Protein C als

C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is a bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction, C:Genetics:

A:Gene: GDB:PROC

A:Cross-references: GDB:120317; OMIM:176860

A:Map position: 2q13-2q21

A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding

F:1-32/Domain: signal sequence #status predicted <SIG>

F:27-86/Domain: Gla domain homology <Gla>

F:33-42/Domain: propeptide #status predicted <PRO>

F:43-197/Product: protein C light chain #status predicted <LCH>

F:92-131/Domain: EGF homology <EG1>

F:140-175/Domain: EGF homology <EG2>

F:200-461/Product: protein C heavy chain #status predicted <HCH>

F:212-445/Domain: trypsin homology <TRY>

F:48-49-56-58-61-62-67-70-76/Modified site: gamma-carboxyglutamic acid (Glu) #status exp

F:59-64-92-105-101-120-122-131-140-151-147-160-162-175-183-319-238-254-373-387-398-426/D

F:106-111/Disulfide bonds: #status predicted

F:110/Binding site: erythro-beta-hydroxyaspartic acid (Asp) #status absent

F:113/Modified site: carboxylate (Thr) (covalent) #status experimental

F:119-290-355/Binding site: carboxylate (Asn) (covalent) #status experimental

F:211-212/Cleavage site: Arg-Leu (Thrombin) #status experimental

F:253-299-402/Active site: His, Asp, Ser #status predicted

F:371/Binding site: carboxylate (Asn) (covalent) (partial) #status atypical

Query Match 84.9%; Score 169; DB 1; Length 461;

Best Local Similarity 72.7%; Pred. No. 1.4e-19;

Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANSFLXLRHSGSLRXRCIXICDFXXAKXIFDVEDDTLAFWSKH 44

DB 43 ANSFLERHSGSLRECEICDFEAKETFGVNDTLAFWSKH 86

RESULT 2

XX0210

protein C (activated) (EC 3.4.21.69) precursor - mouse

N:Alternate names: vitamin K-dependent serine proteinase

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 16-Jun-2000

C:Accession: JX0210

R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.

J. Biochem. 111, 491-495, 1992

A:Title: Isolation and characterization of a mouse protein C cDNA.

A:Reference number: JX0210; MUID:92316897; PMID:1618739

A:Accession: JX0210

A:Molecule type: mRNA

A:Residues: 1-461 <TAB>

A:Cross-references: GB:DI0445; NID:9220385; PIDN:BA01235.1; PID:9220386

A:Experimental source: liver

C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re

S:

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylatant

F:1-33/Domain: signal sequence #status predicted <SIG>

F:27-85/Domain: Gla domain homology <Gla>

F:34-41/Domain: propeptide #status predicted <PRO>

F:42-196-199-461/Product: protein C #status predicted <PC>

F:42-196/Domain: light chain #status predicted <PCD>

F:91-130/Domain: EGF homology <EG1>

F:139-174/Domain: EGF homology <EG2>

F:199-461/Domain: heavy chain #status predicted <PCH>

F:199-211/Domain: activation peptide #status predicted <ACT>

F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

F:212-445/Domain: trypsin homology <TRY>

F:47-48-55-57-60-61-66-67-70-76/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:121-130-139-150-146-159-161-174-182-319-238-254-373-387-398-426/Disulfide bonds: #stat

F:214-290-355/Binding site: carboxylate (Asn) (covalent) #status predicted

F:253-299-402/Active site: His, Asp, Ser #status predicted

Query Match 70.4%; Score 140; DB 1; Length 461;

Best Local Similarity 59.1%; Pred. No. 7.7e-15;

Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANSFLXLRHSGSLRXRCIXICDFXXAKXIFDVEDDTLAFWSKH 44

DB 42 ANSFLERHSGSLRECEICDFEAKETFGVNDTLAFWIKY 85

RESULT 3

S18994

protein C (activated) (EC 3.4.21.69) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 29-Oct-1999

C:Accession: S18994; S24312

R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.

submitted to the EMBL Data Library, February 1992

A:Description: The cDNA cloning and mRNA expression of rat protein C.

A:Reference number: S18994

A:Accession: S18994

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <OKA>

A:Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963

R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.

Biochim. Biophys. Acta 1131, 329-332, 1992

A:Title: The cDNA cloning and mRNA expression of rat protein C.

A:Reference number: S24312; MUID:92329550; PMID:1627650

A:Accession: S24312

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <OKA2>

A:Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol

C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase

F:1-32/Domain: signal sequence #status predicted <SIG>

F:27-85/Domain: Gla domain homology <Gla>

F:33-42/Domain: propeptide #status predicted <PRO>

F:43-461/Product: protein C #status predicted <PC>

F:91-130/Domain: EGF homology <EG1>

F:139-174/Domain: EGF homology <EG2>

F:213-445/Domain: trypsin homology <TRY>

F:47-48-55-57-60-61-66-67-70-76/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:121-130-139-150-146-159-161-174-182-320-239-255-373-387-398-426/Disulfide bonds: #s

F:215-291-355/Binding site: carboxylate (Asp) (covalent) #status predicted

F:254-300-402/Active site: His, Asp, Ser #status predicted

Query Match 69.8%; Score 139; DB 1; Length 461;

Best Local Similarity 59.1%; Pred. No. 1.1e-14;

Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANSFLXLRHSGSLRXRCIXICDFXXAKXIFDVEDDTLAFWSKH 44

DB 42 ANSFLERHSGSLRECEICDFEAKETFGVNDTLAFWIKY 85

RESULT 4

KXBO

protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)

N:Alternate names: autoproteolysin IIA; plasma protein C

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Nov-1980 #sequence-revision 17-Mar-1987 #text-change 16-Jul-1999

C:Accession: A26250; A18385; A18386; A00928

R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984

A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.

A:Reference number: A26250; MUID:85014826; PMID:6091100

A:Accession: A26250

A:Molecule type: mRNA

A:Residues: 1-456 <LON>

R:fernund, P.; Stenflo, J.

J. Biol. Chem. 257, 12170-12179, 1982
A>Title: Amino acid sequence of the light chain of bovine protein C.
A:Reference number: A18385; MUID:83007325; PMID:6896876
A:Accession: A18385
A:Molecule type: protein
A:Residues: 40-194 <PER>
A>Note: 82-Lys was also found
R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A>Title: beta-hydroxyaspartic acid in vitamin K-dependent protein C.
A:Reference number: A19316; MUID:83169769; PMID:6572939
A:Contents: annotation: revision to residue 110
R:Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A>Title: Amino acid sequence of the heavy chain of bovine protein C.
A:Reference number: A18386; MUID:83007326; PMID:6896877
A:Accession: A18386
A:Molecule type: protein
A:Residues: 197-454, 'PV' <SPE>
R:Esmon, N.L.; Debault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A>Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F
A:Reference number: A37541; MUID:8321513; PMID:6304092
A:Contents: annotation: activation: calcium binding
R:Johnson, A.E.; Esmon, N.L.; Lane, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A>Title: Structural changes required for activation of protein C are induced by Ca2+ binding
A:Reference number: A37542; MUID:8321514; PMID:6406503
A:Contents: annotation: activation: calcium binding
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
s:
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this react
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with struc
cognition of the thrombin-thrombomodulin complex.
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F:1-92/Domain: signal sequence (fragment) #status predicted <SIG>
F:24-83/Domain: Gla domain homology <GLA>
F:30-39/Domain: propeptide #status predicted <PRO>
F:40-194/Product: protein C light chain #status experimental <LCH>
F:98-128/Domain: EGF homology <EG3>
F:137-172/Domain: EGF homology <EG2>
F:197-456/Product: protein C heavy chain #status experimental <HCH>
F:197-210/Domain: activation peptide #status experimental <APT>
F:211-440/Domain: trypsin homology <TRY>
F:45, 46, 53, 55, 58, 59, 62, 64, 65, 68, 74/Modified site: gamma-carboxyglutamic acid (Glu) #sta
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:118-128, 137-148, 144-157, 159-172, 180-318, 323-253, 368-382, 393-421/Disulfide bonds: #stat
F:136, 289, 350/Binding site: carboxylate (Asn) (covalent) #status predicted
F:125, 298, 397/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 61.3% Score 122: DB 1: Length 456;
Best Local Similarity 50.0% Pred. No. 6, 7e-12;
Matches 21: Conservative 9; Mismatches 12; Indels 0; Gaps 0;
DB 1 ANSFLXLRHGSILKRXCTIXICDPFXKXKIFZDDVDLTAFWS 42
40 ANSFLLELRPGNVERECSEVECEFEAREIRIIONFTDIAFWWS 81

RESULT 5
EXRT
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
C:Accession: S49075; J04670; P50191; P50190; I62745
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A>Title: Evidence for competition between vitamin K-dependent clotting factors for intrate
A:Reference number: A58498; MUID:96093366; PMID:8578539

[illegible]

A:Cross-references: GB:M2613; NID:g180335; PIDN:AAA51984.1; PID:g180336
R:Funf, M.R.; Hay, C.W.; Macgillivray, R.T.A.
A:Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X.
A:Reference number: A22208; MUID:85216545; PMID:2582420
A:Accession: A22208
A:Molecule type: mRNA
A:Residues: 13-441, 'S', 443-488 <FUN>
A:Cross-references: GB:K03194; NID:g182840; PIDN:AAA52490.1; PID:g182841
R:Leyley, S.P.; Chung, D.W.; Kistiel, W.; Kutrachl, K.; Davle, E.W.
A:Title: Characterization of a cDNA coding for human factor X.
A:Reference number: A21284; MUID:84222026; PMID:6587384
A:Accession: A21284
A:Molecule type: mRNA
A:Residues: 13-284, 'E', 289-488 <LE2>
A:Cross-references: GB:K01886
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howard, W.N.; Kwa, E.Y.; Welns
Biochemistry 22, 2875-2884, 1983
A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.
A:Reference number: A20362; MUID:83257207; PMID:6871167
A:Accession: A20362
A:Molecule type: Protein
A:Residues: 41-179 <MCMC>
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X.
A:Reference number: S39414; MUID:94062825; PMID:823461
A:Accession: S39415
A:Molecule type: Protein
A:Residues: 183-234 <CINO>
A:Note: glycosylation sites
A:Note: Identification and characterization of beta-hydroxyaspartic acid
R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.
Gene 84, 517-519, 1989
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human blood coagulation factor X.
A:Reference number: 154051; MUID:90128299; PMID:2612918
A:Accession: 154051
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-23 <RES>
A:Cross-references: GB:M3297; NID:g183860; PIDN:AAA52636.1; PID:g553330
R:Padmanabhan, K.; Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blumberg, P.M.
J. Mol. Biol. 232, 947-966, 1993
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A:Reference number: A49458; MUID:93360277; PMID:8355279
A:Contents: annotation: X-ray crystallography, 2.2 angstroms
A:Comment: The two chains held together by one disulfide bond are formed from a single-cysteine chain.
A:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or factor XIa (in the extrinsic pathway).
A:Gene: GDB:F10
A:Cross-references: GDB:119890; OMIM:227600
A:Map position: 13q34-13q34
F:1:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A:Note: deficiency of this factor causes Stuart disease
A:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V and calcium ions.
A:Pathway: blood coagulation
C:Keywords: beta-hydroxyaspartic acid, blood coagulation; calcium binding; carboxylglutamic acid
F:1-23/Domain: signal sequence #status predicted <PRO>
F:24-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-179/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EGF1>
F:129-164/Domain: EGF homology <EGF2>
F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F:183-234/Domain: activation peptide #status experimental <APT>
F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F:235-462/Domain: trypsin homology <TRY>
F:46-47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxylglutamic acid (Glu) #status predicted
F:57-62/Disulfide bonds: #status predicted
F:90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-342, 241-246, 261-277, 390-404, 415-443, 457-462, 471-488, 491-500, 503-510, 513-520, 523-530, 533-540, 543-550, 553-560, 563-570, 573-580, 583-590, 593-600, 603-610, 613-620, 623-630, 633-640, 643-650, 653-660, 663-670, 673-680, 683-690, 693-700, 703-710, 713-720, 723-730, 733-740, 743-750, 753-760, 763-770, 773-780, 783-790, 793-800, 803-810, 813-820, 823-830, 833-840, 843-850, 853-860, 863-870, 873-880, 883-890, 893-900, 903-910, 913-920, 923-930, 933-940, 943-950, 953-960, 963-970, 973-980, 983-990, 993-1000, 1003-1010, 1013-1020, 1023-1030, 1033-1040, 1043-1050, 1053-1060, 1063-1070, 1073-1080, 1083-1090, 1093-1100, 1103-1110, 1113-1120, 1123-1130, 1133-1140, 1143-1150, 1153-1160, 1163-1170, 1173-1180, 1183-1190, 1193-1200, 1203-1210, 1213-1220, 1223-1230, 1233-1240, 1243-1250, 1253-1260, 1263-1270, 1273-1280, 1283-1290, 1293-1300, 1303-1310, 1313-1320, 1323-1330, 1333-1340, 1343-1350, 1353-1360, 1363-1370, 1373-1380, 1383-1390, 1393-1400, 1403-1410, 1413-1420, 1423-1430, 1433-1440, 1443-1450, 1453-1460, 1463-1470, 1473-1480, 1483-1490, 1493-1500, 1503-1510, 1513-1520, 1523-1530, 1533-1540, 1543-1550, 1553-1560, 1563-1570, 1573-1580, 1583-1590, 1593-1600, 1603-1610, 1613-1620, 1623-1630, 1633-1640, 1643-1650, 1653-1660, 1663-1670, 1673-1680, 1683-1690, 1693-1700, 1703-1710, 1713-1720, 1723-1730, 1733-1740, 1743-1750, 1753-1760, 1763-1770, 1773-1780, 1783-1790, 1793-1800, 1803-1810, 1813-1820, 1823-1830, 1833-1840, 1843-1850, 1853-1860, 1863-1870, 1873-1880, 1883-1890, 1893-1900, 1903-1910, 1913-1920, 1923-1930, 1933-1940, 1943-1950, 1953-1960, 1963-1970, 1973-1980, 1983-1990, 1993-2000, 2003-2010, 2013-2020, 2023-2030, 2033-2040, 2043-2050, 2053-2060, 2063-2070, 2073-2080, 2083-2090, 2093-2100, 2103-2110, 2113-2120, 2123-2130, 2133-2140, 2143-2150, 2153-2160, 2163-2170, 2173-2180, 2183-2190, 2193-2200, 2203-2210, 2213-2220, 2223-2230, 2233-2240, 2243-2250, 2253-2260, 2263-2270, 2273-2280, 2283-2290, 2293-2300, 2303-2310, 2313-2320, 2323-2330, 2333-2340, 2343-2350, 2353-2360, 2363-2370, 2373-2380, 2383-2390, 2393-2400, 2403-2410, 2413-2420, 2423-2430, 2433-2440, 2443-2450, 2453-2460, 2463-2470, 2473-2480, 2483-2490, 2493-2500, 2503-2510, 2513-2520, 2523-2530, 2533-2540, 2543-2550, 2553-2560, 2563-2570, 2573-2580, 2583-2590, 2593-2600, 2603-2610, 2613-2620, 2623

```

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:129,211/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:221,231/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:234,235/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #s
F:276,322,419/Active site: His Asp, Ser #status experimental

Query Match          53.8% Score 107: DB 1: Length 488:
Best Local Similarity 40.9% Pred. No. 2e-09:
Matches 18: Conservative 9; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGSILKRXICIXICDFXXAKXIFZDDVDLTAFSKH 44
      ||||| ||||| | | | | | | | | | | | | | | | |
Db 41 ANSFLFEKMKKHLRECHMEETCTSEAREVEYEDSDKTNEFNNKY 84

RESULT 8
146932
coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C:Accession: I46932
R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor
A:Reference number: I46932; MUID:93190306; PMID:8383365
A:Accession: I46932
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-443 <BRO>
A:Cross-references: GB:S56300; NID:g266294; PID:g266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
F:24-83/Domain: Gla domain homology <Gla>
F:89-120/Domain: EGF homology <EGF>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match          50.8% Score 101: DB 2: Length 443:
Best Local Similarity 46.3% Pred. No. 1.8e-08:
Matches 19: Conservative 5; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGSILKRXICIXICDFXXAKXIFZDDVDLTAFL 41
      ||||| ||||| | | | | | | | | | | | | | | | |
Db 40 ANSFLLELRPGSLRECKEELCSFEAREVPTSTRTKQFM 80

RESULT 9
KPHU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1999 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
C:Accession: A28332; A23819; A31186; B31186; S63524
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; M
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dep
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OHA>
A:Cross-references: GB:02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965; PMID:3406420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M1322; NID:g182799; PIDN:AAA8040.1; PID:g182801
R:Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen,
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein

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A:Residues: 61-112 <THI>
A:Accession: B31186
A:Molecule type: protein
J.R.Bjornern, S.: Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peder J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations and A:Contents: annotation; carbohydrate binding sites
Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy A:Reference number: S63524; PMID:96096752; PMID:8529655
A:Molecule type: protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence coagulation factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Keywords: beta-hydroxyaspartic acid; EGF homology; Gla domain homology; trypsin homology
F:1-20/Domains: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PRO>
F:45-104/Domains: Gla domain homology <GLA>
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MAL>
F:110-141/Domains: EGF homology <EGF>
F:151-187/Domains: EGF homology <EG2>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domains: trypsin homology <TRY>
F:66-67;74;76;79;80;85;86;89;95/Modified site: gamma-carboxyglutamic acid (Glu) #status F:77-82;110-121;115-130;132-141;151-162;158-172;174-187;195-322;219-224;238-254;370-389,
F:112-120/Binding site: carbonydrate (Ser) (covalent) #status experimental
F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F:205;382/Binding site: carbonydrate (Asn) (covalent) #status experimental
F:212-213/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F:253;302;404/Active site: His_Asp_Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor XIa) #status predicted

Query Match 49.2%; Score 98; DB 1; Length 466;
Best Local Similarity 48.8%; Pred. No. 5.8e+08;
Matches 20; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANSFLXXLRHGSILAKXCIXXICDFXKAXKIFZDVDDTLAFW 41
II::II II III I :: I :: I :: I :: I ::
Db 61 ANAFELELRPGSLERECKEDECSFEARELFKDERTKLFW 101

RESULT 10

KRFBOT
coagulation factor VIIa (BC 3.4.21.21) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C:Accession: A31979; C02274
R:Takaya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
U. Biol. Chem. 263, 14668-14677, 1988
A:Title: Bovine factor VII. Its purification and complete amino acid sequence.
A:Reference number: A31979; PMID:89008362; PMID:3049594
A:Accession: A31979
A:Molecule type: protein
A:Residues: 1-407 <TAK>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.,
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Accession: C20274
A:Molecule type: protein
A:Residues: 58-62; 'X'; 64-68 <MCN>

A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid
R.Hase, S.; Kanabata, S.; Nishimura, H.; Takaya, H.; Sueyoshi, T.; Miyata, T.; Iwanag
J. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood c
A:Reference number: A44556; MUID:89213999; PMID:3149637
A:Contents: annotation
A:Note: structure and location of covalently bound carbohydrate
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
gulation factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA>
F:1-44/Domain: Gla domain homology (fragment) <Gla>
F:50-81/Domain: EGF homology <EG1>
F:91-127/Domain: EGF homology <EG2>
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:153-387/Domain: trypsin homology <TRY>
F:16-7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #sta
F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-3
F:152/Binding site: carbonyldrate (Ser) (covalent) #status experimental
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experim
F:145,203/Binding site: carboxylate (Asn) (covalent) #status experimental
F:152,153/Binding site: Arg-Tile (coagulation factor X) #status experimental
F:193,242,344/Active site: His, Asp, Ser #status predicted
F:190-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 42.2%; Score 84; DB 1; Length 407;
Best Local Similarity 43.9%; Pred. No. 9,86-06;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSGLKRXCIXXICDFYXKXIFZDDDTLAFW 41
||| | ||| | : | | | : | |
Db 1 ANGFLLELPGLSLRECRRELCSFEAAHEIFRNEERTQFW 41

RESULT 11
S10511
thrombin (EC 3.4.21.5) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
C:Accession: S10511; A60576; B42696
R:DiIanich, M.; Monard, D.
Nucleic Acids Res. 18, 4251, 1990
A:Title: cDNA sequence of rat prothrombin.
F:Reference number: S10511; MUID:90332426; PMID:2377469
A:Accession: S10511
A:Molecule type: mRNA
A:Residues: 1-617 <DTH>
A:Cross-references: EMBL:X52835; NID:956969; PIDN:CA437017.1; PID:956970
R:Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus
F:Reference number: A60576; MUID:90091942; PMID:2293980
A:Accession: A60576
A:Molecule type: protein
A:Residues: 44-58 <HEN>
A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat
R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: B42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 383-617, 'E' <BAN>
A:Cross-references: GB:M81397
C:Superfamily: thrombin; Gla domain homology; kinase homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; h
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <Gla>

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 13, 2003, 14:01:08 ; Search time 11 seconds

(without alignments)
165.905 Million cell updates/sec

Title: SEQ1-EDITED

Sequence: 1 ANSFLXLRHGSGLXRXICIX.....XXAKXIFZVDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	169	84.9	461	1	PRTC_HUMAN
2	140	70.4	461	1	PRTC_MOUSE
3	139	69.8	461	1	PRTC_RAT
4	138	69.3	458	1	PRTC_RABIT
5	123	61.8	459	1	PRTC_PIG
6	122	61.3	456	1	PRTC_BOVIN
7	108	54.3	492	1	FA10_BOVIN
8	107	53.8	488	1	FA10_HUMAN
9	107	50.8	231	1	TMG3_HUMAN
10	101	50.8	444	1	FA7_RABIT
11	100	50.3	490	1	FA10_RABIT
12	98	49.2	465	1	FA7_HUMAN
13	86	43.2	218	1	TMG1_HUMAN
14	84	42.2	226	1	TMG4_HUMAN
15	84	42.2	407	1	FA7_BOVIN
16	83.5	42.0	617	1	THRB_RAT
17	83.5	42.0	618	1	THRB_MOUSE
18	81	40.7	622	1	THRB_HUMAN
19	80	40.2	376	1	FA10_TROCA
20	80	40.2	475	1	FA10_CHICK
21	79	39.7	446	1	FA7_MOUSE
22	79	39.7	649	1	PRTS_MACMU
23	79	39.7	676	1	PRTS_HUMAN
24	78	39.2	452	1	FA9_CANFA
25	78	39.2	459	1	FA9_MOUSE
26	78	39.2	446	1	PRTS_RABIT
27	77	38.7	675	1	PRTS_BOVIN
28	74	37.2	461	1	FA9_HUMAN
29	74	35.7	461	1	FA9_BOVIN
30	71	35.7	461	1	THRB_BOVIN
31	69	34.7	625	1	PRTS_MOUSE
32	68	34.2	675	1	PRT2_BOVIN
33	66.5	33.4	396	1	P00744 bos taurus

34	63	31.7	202	1	TMG2_HUMAN	O14669 homo sapien
35	62.5	31.4	400	1	PRT2_HUMAN	P22891 homo sapien
36	50	25.1	501	1	MKCI_CANAL	P43068 candida alb
37	49	24.6	730	1	PRIA_HAEIN	P44647 haemophilus
38	49	24.6	1363	1	VGR1_MOUSE	P35917 mus musculus
39	48	24.1	358	1	ALKJ_PSEOL	O00593 pseudomonas
40	48	24.1	1235	1	CYMA_TRYBB	Q26721 trypanosoma
41	48	24.1	1298	1	VGR3_HUMAN	P35916 homo sapien
42	47	23.6	1343	1	VGR2_RAT	O08775 rattus norv
43	47	23.6	1348	1	VGR2_COTJA	P52583 coturnix co
44	47	23.6	1356	1	VGR2_HUMAN	P35968 homo sapien
45	47	23.6	1367	1	VGR2_MOUSE	P35918 mus musculus

ALIGNMENTS

RESULT 1

ID	PRTC_HUMAN	STANDARD:	PRT:	461 AA.
AC	P04070; O16001; Q15190; Q15189;			
DT	01-NOV-1986 (Rel. 03, Created)			
DT	01-NOV-1986 (Rel. 03, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Vitamin-K dependent protein C precursor (EC 3.4.21.69)			
DE	(Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).			
CN	PROCC.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
NC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85270390; PubMed=2991887;			
RA	Foster D.C., Yoshitake S., Davie E.W.;			
RT	"The nucleotide sequence of the gene for human protein C."			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85269639; PubMed=2991859;			
RA	Beckmann R.J., Schmidt R.J., Santerre R.F., Plutsky J., Crabtree G.R.,			
RT	Long G.L.;			
RL	"The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAs."			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86120978; PubMed=3511471;			
RA	Plutsky J., Hoskins J.A., Long G.L., Crabtree G.R.;			
RT	"Evolution and organization of the human protein C gene."			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Carlington D.P., Chung M.-W., Lee K.L., Pool C.L., Yi Q.,			
RT	Nickerson D.A.;			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 106-461 FROM N.A.			
RX	MEDLINE=84272714; PubMed=6589623;			
RA	Foster D.C., Davie E.W.;			
RT	"Characterization of a cDNA coding for human protein C."			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).			
RN	[6]			
RP	CARBOHYDRATE-LINKAGE SITE ASN-371.			
RX	MEDLINE=90293094; PubMed=1694179;			
RA	Mietlich J.P., Broze G.J. Jr.;			
RT	"Beta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-cysteine sites."			
RL	J. Biol. Chem. 265:11397-11404(1990).			
RN	[7]			

RP HYDROXYLATION.
 RX MEDLINE-92184750; PubMed-1544894;
 RA Harris R.J., Ling V.T., Spellman M.W.;
 RT "O-linked fucose is present in the first epidermal growth factor
 RL domain of factor XII but not protein C.";
 RN J. Biol. Chem. 267:5102-5107(1992).
 (18)
 RP 3D-STRUCTURE MODELING OF 175-450.
 RX MEDLINE-94272342; PubMed-8003977;
 RA Fisher C.L., Greengard J.S., Griffin J.H.;
 RT "Models of the serine protease domain of the human antithrombotic
 RL plasma factor activated protein C and its zymogen.";
 RN Protein Sci. 3:588-599(1994).
 (19)
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
 RX MEDLINE-97157472; PubMed-9003757;
 RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmou C.,
 RA Bode W.;
 RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
 RL EMBO J. 15:6822-6831(1996).
 (110)
 RP REVIEW ON PROC VARIANTS.
 RX MEDLINE-93190290; PubMed-8446940;
 RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
 RA Sala N., Cooper D.N.;
 RT "Protein C deficiency: a database of mutations. For the Protein C & S
 RL Subcommittee of the Scientific and Standardization Committee of the
 RN International Society on Thrombosis and Haemostasis.";
 RN Thromb. Haemost. 69:77-84(1993).
 (111)
 RP VARIANT CYS-444.
 RX MEDLINE-87204221; PubMed-2437584;
 RA Romeo G., Hassan H.T., Staempfli S., Roncuzzi L., Cianetti L.,
 RA Leonard A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
 RA Cortese R.;
 RT "Hereditary thrombophilia: identification of nonsense and missense
 RL mutations in the protein C gene.";
 RN Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
 (112)
 RP VARIANT TRP-211 (LONDON-1).
 RX MEDLINE-90098906; PubMed-2602169;
 RA Grundy C.B., Chitcolle A., Talbot S., Bevan D., Kakkar V.V.,
 RA Cooper D.N.;
 RT "Protein C London 1: recurrent mutation at Arg-169 (CGG->TGC) in
 RL the protein C gene causing thrombosis.";
 RN Nucleic Acids Res. 17:10513-10513(1989).
 (113)
 RP VARIANT CYS-272.
 RX MEDLINE-91329836; PubMed-1868249;
 RA Reitsma P.H., Poort S.R., Allart C.F., Briet E., Bertina R.M.;
 RT "The spectrum of genetic defects in a panel of 40 Dutch families with
 RL symptomatic protein C deficiency type I: heterogeneity and founder
 RN effects.";
 RN Blood 78:890-894(1991).
 (114)
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE-92190481; PubMed-1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillmer E.,
 RA Raluvilla I.R., Long G.L.;
 RT "Protein C Vermont: symptomatic type II protein C deficiency
 RL associated with two Gla domain mutations.";
 RN Blood 79:1456-1465(1992).
 (115)
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE-92305321; PubMed-161081;
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RL deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RN a missense mutation.";
 RN Blood 80:126-133(1992).
 (116)
 RP VARIANT LEU-289.
 RX MEDLINE-92380660; PubMed-1511988;

RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RL causing recurrent venous thrombosis.";
 RN Hum. Genet. 89:683-684(1992).
 (117)
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE-92380661; PubMed-1511989;
 RA Grundy C.B., Schuman S., Tengenborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RL gene causing recurrent venous thrombosis.";
 RN Hum. Genet. 89:685-686(1992).
 (118)
 RP VARIANT GLN-220.
 RX MEDLINE-93250852; PubMed-1301959;
 RA Gandrille S., Vidard M., Atsch M., Alhenc-Gelas M., Fischer A.M.,
 RA Couault-Hellman M., Toulon P., Flessinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 RL deficiency: characterization by denaturing gradient gel
 RN electrophoresis.";
 RN Hum. Mutat. 1:491-500(1992).
 (119)
 RP VARIANT SER-334.
 RX MEDLINE-92276939; PubMed-1593215;
 RA Yamamoto K., Matsushita T., Sugitara I., Takamatsu J., Iwasaki E.,
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RL mutation that causes impaired secretion of the mutant protein C.";
 RN J. Lab. Clin. Med. 119:682-689(1992).
 (120)
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE-93313192; PubMed-8324221;
 RA Gandrille S., Alhenc-Gelas M., Gaussem P., Allard M.-F., Dupuy E.,
 RA Juhan-Vague I., Atsch M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RL gene in patients presenting with defective protein C anticoagulant
 RN activity.";
 RN Blood 82:159-168(1993).
 (121)
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND
 RN V-388.
 RX MEDLINE-93271391; PubMed-8499565;
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RL with hereditary protein C deficiency.";
 RN Blood Coagul. Fibrinolysis 4:273-280(1993).
 (122)
 RP VARIANT TRP-57.
 RX MEDLINE-93271396; PubMed-8499568;
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A Gla domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RL causing type 2 protein C deficiency and recurrent venous
 RN thrombosis.";
 RN Blood Coagul. Fibrinolysis 4:345-347(1993).
 (123)
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.
 RX MEDLINE-94122329; PubMed-8292730;
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 RA Koepfer M.A., Cougulin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 RL symptomatic type I protein C deficiency.";
 RN Blood Coagul. Fibrinolysis 4:791-796(1993).
 (124)
 RP VARIANT SER-423.
 RX MEDLINE-94001606; PubMed-8398832;
 RA Marchetti G., Patrascu P., Gemmati D., Castaman G., Rodeghiero F.,
 RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RL mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RN Br. J. Haematol. 84:285-289(1993).
 (125)
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).


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FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 199 INTERCHAIN (BY SIMILARITY).
FT DISULFID 238 254 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 214 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 387 N-LINKED (IN REF. 2).
FT CONFLICT 328 393 N -> D (IN REF. 2).
FT CONFLICT 393 51945 MW: 53FAAD085B194D6E CRC64;
SQ SEQUENCE 461 AA: 51945 MW: 53FAAD085B194D6E CRC64;

Query Match 70.4%; Score 140; DB 1; Length 461;
Best Local Similarity 59.18; Pred. No. 1,1e-16;
Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANSFLXXLRHGSIXRXICXIXICDFXXAKXIFZVDVDTLAFMSKH 44
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 42 ANSFLFMRGSLRRCMEICDFEFAQELFQVNEDTLAWIKY 85

RESULT 3
PRTC_RAT STANDARD: PRT: 461 AA.
ID PRTC_RAT
AC P31394;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Aucoprothombin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Liver;
RC MEDLINE=92329550; PubMed=1627650;
RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RA "The cdna cloning and mRNA expression of rat protein C.";
RL Biochim. Biophys. Acta 1131:329-332(1992).
CC -I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -I- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADCAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -I- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -I- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: X64336; CAA5617.1; -.
DR PIR: S18994; S18994.
DR PIR: S24312; S24312.
DR HSSP: P04070; IPCU.
DR MEROPS: S01.218; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; Trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM000179; EGF_CA; 1.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_SER; 1.
DR PROSITE: PS00135; TRYPSIN_HIS; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrilase; Signal.
FT SIGNAL 1 32
FT PROPEP 33 41 BY SIMILARITY.
FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 199 461 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT PEPTIDE 212 212 ACTIVATION PEPTIDE (BY SIMILARITY).
FT SITE 212 213 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT DOMAIN 96 131 EGF-LIKE 1.
FT DOMAIN 135 175 EGF-LIKE 2.
FT DOMAIN 213 461 SERINE PROTEASE.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT ACT_SITE 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 254 254 CHARGE RELAY SYSTEM.
FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.

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FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 255 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8AACF93664EDACD5 CRC64;

Query Match 69.8%; Score 139; DB 1; Length 461;
Best Local Similarity 59.1%; Pred. No. 1,6e-16;
Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Oy 1 ANSFLXLRHSGLSRXRCIXICDFXXAKXIFZVDVDTLAFNSKH 44
Db 42 ANSFLFEYRAGSLERECHEICDFEAGCETPQNVEDTLAFWKY 85

RESULT 4
PRTC_RABIT STANDARD: PRT: 458 AA.
AC Q28661:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Antithrombin III) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
GN PROC.
OS Eukaryotes cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Shen L., He X., Dahlback B.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PM: THE VITAMIN K-DEPENDENT ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL: U49933; AAA92956.1; .
CC HSSP: P04070; 1PCU.
CC MEROPS: S01.218; .
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR000561; EGF-like.

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DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin_1.
DR Pfam: PF00594; gla_1.
DR SMART: SM00181; EGF_2.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; tryp_spc_1.
DR PROSITE: PS00010; ASX_HYDROXYL_1.
DR PROSITE: PS00022; EGF_1_1.
DR PROSITE: PS01186; EGF_2_2.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
DR PROSITE: PS50240; TRYPSIN_DOM_1.
DR PROSITE: PS00134; TRYPSIN_HIS_1.
DR PROSITE: PS00135; TRYPSIN_SER_1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT- NON_TER 1 1
FT SIGNAL 1 27
FT PROPEP 28 36
FT CHAIN 37 458
FT CHAIN 37 192
FT CHAIN 195 458
FT PEPTIDE 195 209
FT SITE 209 210
FT DOMAIN 91 126
FT DOMAIN 130 170
FT DOMAIN 210 458
FT MOD_RES 42 42
FT MOD_RES 43 43
FT MOD_RES 50 50
FT MOD_RES 52 52
FT MOD_RES 55 55
FT MOD_RES 56 56
FT MOD_RES 61 61
FT MOD_RES 62 62
FT MOD_RES 65 65
FT MOD_RES 107 107
FT ACT_SITE 250 250
FT ACT_SITE 286 296
FT ACT_SITE 399 399
FT ACT_SITE 53 58
FT DISULFID 86 105
FT DISULFID 95 100
FT DISULFID 99 114
FT DISULFID 116 125
FT DISULFID 134 145
FT DISULFID 141 154
FT DISULFID 156 169
FT DISULFID 177 316
FT DISULFID 235 251
FT DISULFID 370 384
FT DISULFID 393 423
FT CARBOHYD 133 133
FT CARBOHYD 287 287
FT CARBOHYD 352 352
SQ SEQUENCE 458 AA; 51087 MW;
Query Match 69.3%; Score 138; DB 1; Length 458;
Best Local Similarity 59.1%; Pred. No. 2,4e-16;
Matches 26; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

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OY 1 ANSFLXHLHSGSLXRXICXICDFXXAKXIFZVDVDTLAFWSKH 44
DB 37 ANSFLEELRPSLSREBCEVGVCDLEAKEIFQSVDDTLAFWKY 80

RESULT 5
PRTC_PIG STANDARD; PRT; 459 AA.
ID PRTC_PIG
AC 09GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysis) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; Pubmed=11229814;
RA Grimm D.R., Collier M.B., Braunschweig M., Alexander L.J., Neame P.J.,
RA Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modeling of membrane binding sites and comparative anatomy of
RT domains."
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -i- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIa
CC in the presence of calcium ions and phospholipids.
CC -i- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -i- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -i- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -i- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -i- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the Gla domain. This Gla-independent binding
CC site is necessary for the recognition of the
CC thrombin-thrombomodulin complex.
CC -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -i- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL: AF191307; AAC28380.1; -
CC HSSP: P04070; 1PCU.
CC MEROPS: S01.218; -
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR001881; EGF_Ca.
CC InterPro: IPR002383; Gla_blood.
CC InterPro: IPR001254; Ser_protease_Try.
CC InterPro: IPR000294; Vltk_dep_Gla.
CC Pfam: PF00008; EGF_2.
CC Pfam: PF00089; trypsin_1.
CC Pfam: PF00594; gla_1.
DR

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DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00001; EGF_Like_2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 18
FT PROPEP 19 41
FT CHAIN 42 459
FT CHAIN 42 196
FT CHAIN 199 459
FT PEPTIDE 199 213
FT SITE 213 214
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 214 459
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 255 255
FT ACT_SITE 301 301
FT ACT_SITE 400 400
FT ACT_SITE 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 321
FT DISULFID 240 256
FT DISULFID 371 385
FT DISULFID 396 424
FT CARBOHD 138 138
FT CARBOHD 292 292
FT CARBOHD 353 353
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC1ACCI6D09 CRC64;

Query Match 61.8%; Score 123; DB 1; Length 459;
Best Local Similarity 52.3%; Pred. No. 1e-13;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

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FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 180 318 INTERCHAIN.
FT DISULFID 237 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .)
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .)
FT VARIANT 82 82 F -> K.
FT CONFLICT 455. 456 VP -> PV (IN REF. 4).
SQ SEQUENCE 456 AA; 51407 MW; CAAFE833F894CC209 CRC64;

Query Match 61.3%; Score 122; DB 1; Length 456;
Best Local Similarity 50.0%; Pred. No. 1.5e-13;
Matches 21; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSIXRXIXXICDFXKAKXIFZDVDTLAWMS 42
Db 40 ANSFLELRPGNWERECSECEFEARELIFONTEDTMAWMS 81

RESULT 7
FA10_BOVIN STANDARD; PRT; 492 AA.
ID FA10_BOVIN
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN 11
RX SEQUENCE OF 1-487 FROM N.A.
RA MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence."
RL Nucleic Acids Res. 12:4461-4492(1984).
RN 12
RX SEQUENCE OF 41-180.
RA MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN 13
RX REVISION TO 103.
RA MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens."
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN 14
RX SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RA MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN 15
RX SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RA MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";

RL Eur. J. Biochem. 218:153-163(1993).
[6]
RX ACTIVE SITE.
RA MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN 17
RX PROCESSING.
RA MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN 18
RX CALCIUM-BINDING DATA.
RA MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN 19
RX SULFATION.
RA MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN 110
RX STRUCTURE BY NMR OF 85-126.
RA MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
RL Biochemistry 29:8111-8118(1990).
RN 111
RX STRUCTURE BY NMR OF 85-126.
RA MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).
RN 112
RX STRUCTURE BY NMR OF 85-126.
RA MEDLINE=92406922; PubMed=1527084;
RA Selander M., Ullner M., Persson E., Telemann O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X.";
RL J. Biol. Chem. 267:19642-19649(1992).
RN 113
RX STRUCTURE BY NMR OF 41-126.
RA MEDLINE=96387194; PubMed=8794734;
RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
RA Tremhella J.;
RT "The relative orientation of Gla and EGF domains in coagulation
RT factor X is altered by Ca2+ binding to the first EGF domain. A
RT combined NMR-small angle X-ray scattering study.";
RL Biochemistry 35:11547-11559(1996).
RN 114
RX FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
RX converts prothrombin to thrombin in the presence of factor Va,
RX calcium and phospholipid during blood clotting.
RN 115
RX CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then
RX Arg-1-Ile bonds in prothrombin to form thrombin.
RN 116
RX SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
RX BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR

```


RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 RP [7]
 RN SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RA MEDLINE=94062825; PubMed=8243461;
 RX Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [8]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Cardin A.D., Kissel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 233:947-966(1993).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 CC -I- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -I- PTM: N- AND O-GLYCOSYLATED.
 CC -I- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: K03194; AAA52490.1; -;
 DR EMBL: M57285; AAA52421.1; -;
 DR EMBL: L29433; AAA52764.1; -;
 DR EMBL: L00390; AAA52764.1; JOINED.
 DR EMBL: L00391; AAA52764.1; JOINED.
 DR EMBL: L00392; AAA52764.1; JOINED.
 DR EMBL: L00393; AAA52764.1; JOINED.
 DR EMBL: L00394; AAA52764.1; JOINED.
 DR EMBL: L00395; AAA52764.1; JOINED.
 DR EMBL: L00396; AAA52764.1; JOINED.
 DR EMBL: M2613; AAA51984.1; -;
 DR EMBL: K01866; AAA52486.1; -;
 DR EMBL: M33297; AAA52636.1; -;
 DR PIR: A00924; EXHU.
 DR PIR: A25853; A25853.
 DR PIR: A24478; A24478.
 DR PDB: 1HCG; 08-MAY-95.

DR PDB: 1FAX; 29-OCT-97.
 DR PDB: 1EXY; 17-JUN-98.
 DR PDB: 1XKA; 23-MAR-99.
 DR PDB: 1XKB; 23-MAR-99.
 DR MEROPS: S01_216; -;
 DR GlycoSuiteDB: P00742; -;
 DR Genew: HGNC:3528; F10.
 DR MIM: 134530; -;
 DR MIM: 227600; -;
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_Like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein. Hydrolase. Serine protease. Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium binding; Vitamin K;
 KW Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
 FT SIGNAL 1 31
 FT PROPEP 32 40
 FT CHAIN 41 179
 FT CHAIN 183 488
 FT PROPEP 183 224
 FT CHAIN 235 422
 FT DOMAIN 86 128
 FT DOMAIN 125 165
 FT DOMAIN 235 488
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 FT MOD_RES 56 56
 FT MOD_RES 59 59
 FT MOD_RES 60 60
 FT MOD_RES 65 65
 FT MOD_RES 66 66
 FT MOD_RES 69 69
 FT MOD_RES 72 72
 FT MOD_RES 79 79
 FT MOD_RES 103 103
 FT MOD_RES 199 199
 FT CARBOHYD 211 211
 FT CARBOHYD 221 221
 FT CARBOHYD 231 231
 FT ACT_SITE 276 276
 FT ACT_SITE 322 322
 FT ACT_SITE 419 419
 FT DISULFID 90 101
 FT DISULFID 95 110
 FT DISULFID 112 121
 FT DISULFID 129 140
 Query Match 53.8%; Score 107; DB 1; Length 488;

DR PROSITE: PS01187; EGF_CA: 1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM: 1.
 DR PROSITE: PS00134; TRYPSIN_HIS: 1.
 DR PROSITE: PS00135; TRYPSIN_SER: 1.
 KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 21
 FT PROPEP 22 39
 FT CHAIN 40 191
 FT CHAIN 192 444
 FT DOMAIN 45 74
 FT DOMAIN 85 121
 FT DOMAIN 126 167
 FT DOMAIN 192 444
 FT SITE 191 192
 FT ACT_SITE 232 232
 FT ACT_SITE 281 281
 FT ACT_SITE 383 383
 FT BINDING 377 377
 FT DISULFID 56 61
 FT DISULFID 89 100
 FT DISULFID 94 109
 FT DISULFID 111 120
 FT DISULFID 130 141
 FT DISULFID 137 151
 FT DISULFID 153 166
 FT DISULFID 174 301
 FT DISULFID 198 203
 FT DISULFID 217 233
 FT DISULFID 349 368
 FT DISULFID 379 407
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 FT MOD_RES 46 46
 FT MOD_RES 53 53
 FT MOD_RES 55 55
 FT MOD_RES 58 58
 FT MOD_RES 59 59
 FT MOD_RES 64 64
 FT MOD_RES 65 65
 FT MOD_RES 68 68
 FT MOD_RES 74 74
 FT MOD_RES 102 102
 FT MOD_RES 211 211
 FT CARBOHD 242 242
 FT CARBOHD 306 306
 FT SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;
 Query Match 50.8%; Score 101; DB 1; Length 444;
 Best Local Similarity 46.3%; Pred. No. 7, 2e-10;
 Matches 19; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGLSRXCIXICDFXAKKIFDQDDTLAFW 41
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 DB 40 ANSFLRLRPGSLRCKELCSFEAREVFQSTERTKQW 80

RESULT 11
 ID FA10_RABIT STANDARD; PRT; 490 AA.
 AC 019045;
 DT 15-DEC-1998 (rel. 37, last sequence update)
 DT 15-DEC-1998 (rel. 37, last sequence update)
 DT 15-JUN-2002 (rel. 41, last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]

RP SEQUENCE FROM N.A.
 RA MEDLINE=97256311; PubMed=9101642;
 RX Pendurthi U.R., Anderson K.D., James H.L.;
 RT "Characterization of a full-length cDNA for rabbit factor X."; Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then Arg-1-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY) (BY SIMILARITY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: AF003200; AB62542.1; -
 DR HSSP: P00742; 1HCG.
 DR MEROPS: S01.216; -
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin_1.
 DR Pfam: PF00594; gla_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA: 1.
 DR SMART: SM00001; EGF_like: 1.
 DR SMART: SM00069; GLA: 1.
 DR SMART: SM00020; Tryp_Spc: 1.
 DR PROSITE: PS00010; ASX-HYDROXYL: 1.
 DR PROSITE: PS00022; EGF_1: 1.
 DR PROSITE: PS01186; EGF_2: 2.
 DR PROSITE: PS01187; EGF_CA: 1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM: 1.
 DR PROSITE: PS00134; TRYPSIN_HIS: 1.
 DR PROSITE: PS00135; TRYPSIN_SER: 1.
 KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KW Signal; Zymogen; EGF-like domain; Repeat.
 FT SIGNAL 1 20
 FT PROPEP 21 40
 FT CHAIN 41 180
 FT CHAIN 184 490
 FT PROPEP 184 232
 FT CHAIN 233 480
 FT DOMAIN 86 122
 FT DOMAIN 125 165
 FT DOMAIN 233 490
 FT BY SIMILARITY.
 FT FACTOR X LIGHT CHAIN.
 FT FACTOR X HEAVY CHAIN.
 FT ACTIVATION PEPTIDE.
 FT ACTIVATED FACTOR XA, HEAVY CHAIN.
 FT EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT EGF-LIKE 2.
 FT SERINE PROTEASE.

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FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 47 47 SIMILARITY).
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 56 56 SIMILARITY).
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 60 60 SIMILARITY).
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 66 66 SIMILARITY).
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.
FT ACT_SITE 320 320 CHARGE RELAY SYSTEM.
FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
FT DISULFID 259 275 BY SIMILARITY.
FT DISULFID 388 402 BY SIMILARITY.
FT DISULFID 413 441 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 490 AA: 53965 MM: 3A39FA85AF2A6D11 CRC64:

Query Match 50.3%: Score 100: DB 1: Length 490:
Best Local Similarity 40.9%: Pred. 1.2e-01:
Matches 18: Conservative 9: Mismatches 17: Indels 0: Gaps 0:

OY 1 ANSFLXLRHGLRXCIXXICDFXAKKIFZDVDDTLAFMSKH 44
Db 41 ANSFLEELKKGNLEBCECMENCSYEALVEFEDREKTNEMWNY 84

RESULT 12
FA7_HUMAN STANDARD: PRT: 466 AA.
AC P08709: Q14339:
DT 01-JUN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (BC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurechi K.,

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RA Davie E.W.;
RA "Characterization of a cDNA coding for human factor VII.";
RA Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RL directed mutagenesis of serine 52 to alanine.";
RN [6]
RP J. Biol. Chem. 266:11051-11057(1991).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimomishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RN [7]
RX J. Biol. Chem. 264:20320-20325(1989).
RN [8]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RN [8]
RX Adv. Exp. Med. Biol. 281:121-131(1990).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.R., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RN [9]
RX Nature 380:41-46(1996).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126538; PubMed=9925787;
RA Zhang E., St. Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPTI mutant.";
RN [10]
RX J. Mol. Biol. 285:2089-2104(1999).
RN [11]
RP STRUCTURE BY NMR OF 105-145.
RX MEDLINE=98367502; PubMed=9692950;
RA Murayai A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
RA Drakenberg T.;
RT "Solution structure of the N-terminal EGF-like domain from human
RT factor VII.";
RX Biochemistry 37:10605-10615(1998).

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[11]
RP VARIANT GLN-364.
RX MEDLINE=91300046; PubMed=20700047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RT Maede T.W., Tuddenham E.G.D.;
RT "Purification and characterisation of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RT male.";
RL Blood 78:132-140(1991).
RN [12]
RP VARIANTS GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=16334227;
RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo G., Casarotto A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterisation of a repeat
RT polymorphism in the factor VII gene (F7).";
RL Hum. Genet. 89:497-502(1992).
RN [13]
RP VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544;
RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;
RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
RT (115His and 333Ser) in the human coagulation factor VII gene.";
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [14]
RP VARIANTS.
RX MEDLINE=94061028; PubMed=8242057;
RA Takamiya O., Kembhall-Cook G., Marin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of
RT coagulation factor VII.";
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [15]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94264305; PubMed=8204879;
RA Chaign S., Clarke B., Sridhara S., Chu K., Friedman P., Vandsusen W.,
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
RT cleavage site for activation and altering binding to tissue factor.";
RL Blood 83:3524-3535(1994).
RN [16]
RP VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7981691;
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
RT factors VII (299Ala-->Val) and X (334Ser-->Pro).";
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [17]
RP VARIANT MIE HIS-307.
RX MEDLINE=95064662; PubMed=7974346;
RA Ohiwa M., Hayaashi T., Wada H., Minamikawa K., Shirakawa S.,
RA Suzuki K.;
RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by
RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
RT catalytic domain.";
RL Thromb. Haemost. 71:773-777(1994).
RN [18]
RP VARIANT MET-419.
RX MEDLINE=96247510; PubMed=8652821;
RA Ardini A.A., Mannucci P.M., Bauer K.A.;
RT "A Thr35Met mutation in factor VII of a patient with a hereditary
RT deficiency causes defective secretion of the molecule.";
RL Blood 87:5085-5094(1996).
RN [19]
RP VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
RX MEDLINE=97001216; PubMed=8844208;
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G.;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII
RT deficiency.";

Hum. Mutat. 8:108-115(1996).

[20]

VARIANT VAL-304.

RX MEDLINE=97037613; PubMed=8883260;

RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,

RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,

RA Zaizov R., Seligson U.;

DE "A1a24Val is a common, probably ancient mutation causing factor VII

RT deficiency in Moroccan and Iranian Jews.";

RL Thromb. Haemost. 76:283-291(1996).

RN [21]

RP VARIANTS MALTA THR-194 AND VAL-304.

RX MEDLINE=98112461; PubMed=9452082;

RA Alshinawi C., Scerril C., Gaidels R., Aquillina A., Felice A.E.;

RT "Two new missense mutations (P134T and A244V) in the coagulation

RL factor VII gene.";

RN Hum. Mutat. Suppl. 1:S189-S191(1998).

CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS

CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR

CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR

CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA

CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO

CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.

CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-I-Ile bond in factor X'co

CC form factor xa.

CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED

CC BY A DISULFIDE BOND.

CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are

CC produced by alternative splicing.

CC -I- TISSUE SPECIFICITY: PLASMA.

CC -I- PIM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME

CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CC CALCIUM.

CC -I- DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.

CC -I- PHARMACEUTICAL: Available under the names Niastase or Novoseven

CC (Novo Nordisk). Used for the treatment of bleeding episodes in

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use.

RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol., 281:121-131(1990).

```

CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-1-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERO DIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC PIR: A31979; A31979.
CC HSSP: P08709; 1BF9.
CC MEROPS: S01.215; -.
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR000742; EGF_2.
CC InterPro: IPR001881; EGF_Ca.
CC InterPro: IPR001438; EGF_II.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR001254; Ser_protease_Try.
CC InterPro: IPR000294; Vitk_dep_GLA.
CC Pfam: PF00008; EGF_2.
CC Pfam: PF00089; trypsin; 1.
CC Pfam: PF00594; gla; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00010; EGFBL00D.
CC PRINTS: PR00001; GLABLOOD.
CC SMART: SM00179; EGF_CA; 1.
CC SMART: SM00001; EGF_Like; 1.
CC SMART: SM00069; GLA; 1.
CC SMART: SM00020; TRYF_SPC; 1.
CC PROSITE: PS00010; ASX_HYDROXYL; 1.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01186; EGF_2; 2.
CC PROSITE: PS01187; EGF_CA; 1.
CC PROSITE: PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE: PS00240; TRYPSIN_DOM; 1.
CC PROSITE: PS00134; TRYPSIN_HIS; 1.
CC PROSITE: PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
CC Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
CC EGF-like domain; Repeat.
CC CHAIN 1 152
CC FT CHAIN 153 407
CC FT DOMAIN 6 35
CC FT DOMAIN 46 82
CC FT DOMAIN 87 128
CC FT DOMAIN 153 407
CC FT SITE 152 153
CC FT ACT_SITE 193 193
CC FT ACT_SITE 242 242
CC FT ACT_SITE 344 344
CC FT BINDING 338 338
CC FT DISULFID 17 22
CC FT DISULFID 50 61
CC FT DISULFID 55 70
CC FT DISULFID 72 81
CC FT DISULFID 91 102
CC FT DISULFID 98 112
CC FT DISULFID 114 127
CC FT DISULFID 135 262
CC FT DISULFID 159 164
CC FT DISULFID 178 194
CC FT DISULFID 310 329
CC FT DISULFID 340 368

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FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 52 52 O-LINKED (GLC. . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636FF7F10 CRC64;

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Query Match 42.2%; Score 84; DB 1; Length 407;
Best Local Similarity 43.9%; Pred. No. 6; 4e-07;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

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QY 1 ANSFLXLRHGSIXRCIXIXICDFXXAKXIFZDVDDTLAFW 41
| | | | | | | | | | | | | | | | | | | |
Db 1 ANGFLLELLPGSLERECREELCSFEENHLEFRNEERTROFW 41

```

Search completed: May 13, 2003, 14:03:33
 Job time : 12 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 13, 2003, 14:01:48 : Search time 29 Seconds

(without alignments)
312.623 Million cell updates/sec

Title: SEQ1-EDITED

Perfect score: 199
Sequence: 1 ANSFLXLRHGLKXRCIXX.....XXAKXIFZVDVDTLAFMSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	75.9	456	09TTRO	09TTRO canis fam1
2	140	70.4	460	091WN8	091WN8 mus musculu
3	134	67.3	460	099PC6	099PC6 mus musculu
4	112	56.3	482	063207	063207 rattus norv
5	98	49.2	481	054740	054740 mus musculu
6	98	49.2	481	099L32	099L32 mus musculu
7	98	49.2	481	088947	088947 mus musculu
8	98	49.2	701	096R08	096R08 homo sapien
9	92	46.2	469	096MD9	096MD9 orlithorhyn
10	92	46.2	100	015253	015253 homo sapien
11	79	39.7	446	061109	061109 mus musculu
12	79	39.7	650	09NSD0	09NSD0 homo sapien
13	79	39.7	650	016519	016519 homo sapien
14	76.5	38.4	542	08T613	08T613 halocynthia
15	76	38.2	138	028994	028994 sus scrofa
16	75	37.7	607	091001	091001 gallus gall

17	74	37.2	456	4	014316	014316 homo sapien
18	74	37.2	461	6	095ND7	095ND7 pan troglod
19	74	37.2	461	6	095ND6	095ND6 pan troglod
20	72	36.2	648	6	029094	029094 sus scrofa
21	71.5	35.9	433	13	0290K1	0290K1 brachydanto
22	71	35.7	49	6	095ME8	095ME8 bos taurus
23	70	35.2	98	13	P82807	P82807 notechis sc
24	69	34.7	608	13	09PTW7	09PTW7 struthio ca
25	67	33.7	399	11	09COM3	09COM3 mus musculu
26	64	32.2	25	11	09OVH6	09OVH6 rattus sp.
27	63	31.7	179	4	08TRAS3	08TRAS3 homo sapien
28	63	31.7	198	11	08RI82	08RI82 mus musculu
29	59	29.6	673	11	061592	061592 mus musculu
30	59	29.6	674	11	099K57	099K57 mus musculu
31	58	29.1	674	11	063772	063772 rattus sp.
32	57	28.6	678	4	014393	014393 homo sapien
33	56.5	28.4	606	10	09SUG9	09SUG9 arabidopsis
34	56.5	28.4	651	10	08S218	08S218 oryza sativ
35	55.5	27.9	459	10	09SE22	09SE22 oryza sativ
36	55.5	27.9	575	10	094E17	094E17 oryza sativ
37	54.5	27.4	603	10	09LPG7	09LPG7 arabidopsis
38	53.5	26.9	196	10	004284	004284 selaginella
39	53.5	26.9	567	10	08W4J2	08W4J2 arabidopsis
40	53.5	26.9	593	10	09LUC3	09LUC3 arabidopsis
41	53.5	26.9	608	10	09XF36	09XF36 medicago sa
42	52.5	26.4	431	10	094EY5	094EY5 arabidopsis
43	52.5	26.4	506	10	09SPF0	09SPF0 oryza sativ
44	52.5	26.4	506	10	09SE23	09SE23 oryza sativ
45	52.5	26.4	543	10	09MB23	09MB23 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q9TTRO	PRELIMINARY	PRT	456 AA.
AC	Q9TTRO			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Protein C precursor.			
GN	PROC.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Leeb T., Kopp T., Deppe A., Breen M., Matls U., Brunnberg L.,			
RA	Brenig B.;			
RT	"Molecular characterization and chromosomal assignment of the canine			
RT	protein C gene."			
RL	Mamm. Genome 10:135-139(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99371952; PubMed=10443005;			
RA	Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;			
RT	"Analysis of canine protein C gene polymorphisms."			
CC	Anim. Genet. 30:237-238(1999).			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE			
CC	TRYPSIN FAMILY.			
CC	EMBL: AJ001979; CAA05126.1; -			
DR	HSSP: P04070; IPCU.			
DR	MEROPS: S01.218; -			
DR	InterPro: IPR000152; Asx_hydroxyl.			
DR	InterPro: IPR001314; Chymotrypsin.			
DR	InterPro: IPR000561; EGF-like.			
DR	InterPro: IPR001881; EGF Ca.			
DR	InterPro: IPR002383; GLA_blood.			
DR	InterPro: IPR001254; Ser_protease_Try.			
DR	InterPro: IPR00294; Vitr_dep_GLA.			
DR	Pfam: PF00008; EGF; 2.			

DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00065; GLA; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00010; ASX-HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Calcium-binding: EGF-like domain; Glycoprotein; Hydrolase;
 KW Hydroxylation; Repeat; Serine protease; Signal.
 FT SIGNAL 1 42
 FT CHAIN 43 192 POTENTIAL.
 FT CHAIN 193 194 PROTEIN C LIGHT CHAIN.
 FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.
 SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 75.9%; Score 151; DB 6; Length 456;
 Best Local Similarity 63.6%; Pred. No. 1.2e-17;
 Matches 28; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGSIXRCIXXICDFXXAKXIFZDVDDTLAFWSKH 44
 DB 43 ANSFLFMRGSLERECMEICDFEAKELFQNVEDTLAFWKY 86

RESULT 2

O91WN8 PRELIMINARY; PRT; 460 AA.
 AC O91WN8.
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Similar to protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC013896; AAH13896.1; -.
 DR MGD: MGI:97771; Proc.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PROSITE: PS00010; ASX-HYDROXYL; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE: PS01187; EGF_CA; UNKNOWN_1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; UNKNOWN_1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;

Query Match 70.4%; Score 140; DB 11; Length 460;
 Best Local Similarity 59.1%; Pred. No. 9.6e-16;

Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 OY 1 ANSFLXLRHGSIXRCIXXICDFXXAKXIFZDVDDTLAFWSKH 44
 DB 42 ANSFLFMRGSLERECMEICDFEAKELFQNVEDTLAFWKY 85

RESULT 3

O99PC6 PRELIMINARY; PRT; 460 AA.
 AC O99PC6.
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Anticoagulant protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Korf I.;
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RL -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC EMBL: AF318182; AKK07918.1; -.
 DR HSSP: P04070; IPCU.
 DR MEROPS: S01.218; -.
 DR MGD: MGI:97771; Proc.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00001; EGF-like; 2.
 DR SMART: SM00065; GLA; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00010; ASX-HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding: EGF-like domain; Glycoprotein; Hydrolase;
 KW Hydroxylation; Repeat; Serine protease.
 SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

Query Match 67.3%; Score 134; DB 11; Length 460;
 Best Local Similarity 56.8%; Pred. No. 1.1e-14;
 Matches 25; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGSIXRCIXXICDFXXAKXIFZDVDDTLAFWSKH 44
 DB 42 ANSFLFMRGSLERECMEICDFEAKELFQNVEDTLAFWKY 85

RESULT 4

O63207 PRELIMINARY; PRT; 482 AA.
 AC O63207;

```

DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE-96093366; PubMed-8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase."
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL: X79807; CAA56202.1; -.
CC DR HSSP: P00742; 1XKA.
CC DR MEROPS: S01.216; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; gla_1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
KW Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 56.3%; Score 112; DB 11; Length 482;
Best Local Similarity 40.9%; Pred. No. 7.5e-11;
Matches 18; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE-98454993; PubMed-9783672;
RA Heidmann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X."
RT Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL: AJ22677; CAA10933.1; -.
CC DR HSSP: P00742; 1XKA.
CC DR MEROPS: S01.216; -.
CC DR MGD: MGI:103107; F10.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00089; EGF_2.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; gla_1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW Signal.
KW SIGNAL.
FT CHAIN 1 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702D5E9F9D97AE CRC64;

Query Match 49.2%; Score 98; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 2e-08;
Matches 16; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

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OY 1 ANSFLLXLRHGSIXRXCIXXICDPFXAKXIFZVDVDTLAFMSKH 44
DB 41 ANSFPEIKKGNLRECEVEICSFEEAREYFEDNEKTTETWMTY 84

RESULT 5
054740 PRELIMINARY: PRT; 481 AA.
AC 054740;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
DE F10 OR F10.
CN F10.
OS Mus musculus (Mouse).
OG Plasmid pluescript.
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RX Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

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OY 1 ANSFLLXLRHGSIXRXCIXXICDPFXAKXIFZVDVDTLAFMSKH 44
DB 41 ANSFPEIKKGNLRECEVEICSFEEAREYFEDNEKTTETWMTY 84

RESULT 6
099132 PRELIMINARY: PRT; 481 AA.
AC 099132;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Coagulation factor X.
DE F10.
CN F10.
OS Mus musculus (Mouse).
OG Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RX Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

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DR	PROSITE: PS0240; TRYPSIN_DOM; 1.
DR	PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR	PROSITE: PS00135; TRYPSIN_SER; 1.
KW	Hydrolase; Serine protease.
SO	SEQUENCE 469 AA; 52196 MW; 4666C230D0758F6A CMC64;
Query Match	
Best Local Similarity	46.2%; Score 92; DB 6; Length 469;
Matches 16; Conservative	7; Mismatches 19; Indels 0; Gaps 0;
OY	1 ANSFLXLRHGSLSXKXCIXIXICDPFXAKXIXI2DVDDTLAFPS 42
DB	41 ANSLFEELKGNLERECNEETCSYEAREVEDDXTNEFWN 82
RESULT 10	
ID	Q15253 PRELIMINARY; PRT; 100 AA.
AC	Q15253;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Thrombin precursor (Fragment).
GN	F2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=87182874; PubMed=3471151;
RT	MacGillivray R.T., Irwin D.M., Guinco E.R., Stone J.C.;
RT	"Recombinant genetic approaches to functional mapping of thrombin.";
RL	Ann. N. Y. Acad. Sci. 485:73-79(1986).
DR	EMBL; M3031; AAA60220.1; -.
DR	InterPro: IPR002383; GLA_blood.
DR	InterPro: IPR000294; Vitk_dep_GLA.
DR	Pfam: PF00594; gla; 1.
DR	PRINTS; PR00001; GLABLOOD.
DR	SMART; SM0069; GLA; 1.
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW	Signal.
FT	SIGNAL 1 43 POTENTIAL.
FT	CHAIN 44 >100 POTENTIAL.
FT	NON_TER 100 100
SO	SEQUENCE 100 AA; 11302 MW; FD0E5D0174E16FE CRC64;
Query Match	
Best Local Similarity	40.7%; Score 81; DB 4; Length 100;
Matches 15; Conservative	8; Mismatches 21; Indels 0; Gaps 0;
OY	1 ANSFLXLRHGSLSXKXCIXIXICDPFXAKXIXI2DVDDTLAFPSKH 44
DB	44 ANTLFEELKGNLERECNEETCSYEAREVEALESSTATDVFWAKY 87
RESULT 11	
ID	Q61109 PRELIMINARY; PRT; 446 AA.
AC	Q61109;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Coagulation factor VII.
GN	F7 OR FVII.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RT	Tissue=Liver.

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RX MEDLINE=96276538; PubMed=8701412;
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RT Thromb. Haemost. 75:481-487(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: U44795; AAC52570.1; -
DR HSSP: P08709; 1FAK.
DR MEROPS: S01.215; -.
DR MGD: MGI:109325; F7.
DR InterPro: IPR002086; Aldohyde_dehydr.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF-like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_SIT; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Calcium-binding: EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 39.7%; Score 79; DB 11; Length 446;
Best Local Similarity 43.9%; Pred. No. 3.8e-05;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGSILXRXCIXICDFXAKKXIFZVDVDTLAFW 41
DB 42 ANSLEELMPGSLERECNEQCSFEARERIFKSPERTKQFW 82

RESULT 12
OQNSDO PRELIMINARY: PRT: 650 AA.
AC OQNSDO:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Protein S precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
[1]
RN TISSUE=LIVER;
RC TISSUE=LIVER;
RA Wydio R., Cohen E., Dackowski W., Stenflo J., Lundwall A.,
RA Dahlback B.;
RL Submitt. (FEB-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: X12892; CAA31383.1; -.
DR HSSP: P00740; 1CFH.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.

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DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 2.
DR Calcium-binding: EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 650 POTENTIAL.
SQ SEQUENCE 650 AA; 72480 MW; C67345CE8645174 CRC64;

Query Match 39.7%; Score 79; DB 4; Length 650;
Best Local Similarity 34.1%; Pred. No. 5.7e-05;
Matches 15; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANSFLXLRHGSILXRXCIXICDFXAKKXIFZVDVDTLAFWSKH 44
DB 16 ANSLEETKQGLNERCEIEELCNKEAREVENDPEITDFYFKY 59

RESULT 13
OQ16519 PRELIMINARY: PRT: 650 AA.
AC OQ16519:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Protein S precursor (Fragment).
GN ProS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86313649; PubMed=2944113;
RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydio R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
RT of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
DR EMBL: M14338; AAA60181.1; -.
DR HSSP: P00740; 1CFH.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00282; LamG; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR Calcium-binding: EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW

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KW Signal.
FT NON_TER 1 1
FT SIGNAL. <1 15 POTENTIAL.
FT CHAIN 16 650 PROTEIN S
SQ SEQUENCE 650 AA: 72462 MW: 9A8C044C503BF474 CRC64;

Query Match
Best Local Similarity 39.7%; Score 79; DB 4; Length 650;
Best Local Similarity 34.1%; Pred. No. 5.7e-05;
Matches 15; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

OY 1 ANSFLXXLRHGSIXRXICIXICFPXAXKIFZDVDDTLAFWSKH 44
DB 16 ANSLLEETKOGNLERECIEELCKNEAREVFEENDPETYFYPKY 59

RESULT 14
O8T613
ID 08T613 PRELIMINARY: PRT: 542 AA.
AC 08T613;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Gla-like protein.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang C.-P., Stafford D.W.;
RT "Halocynthia roretzi gla-like protein partial genomic DNA sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF466701; AAL74247.2;
SQ SEQUENCE 542 AA: 62090 MW: EB9BF13FE42B32FE CRC64;

Query Match
Best Local Similarity 38.4%; Score 76.5; DB 5; Length 542;
Best Local Similarity 30.2%; Pred. No. 0.00013;
Matches 13; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

OY 3 SFLXLRHGSIXRXICIXICDPXAXKIFZ-DVDDTLAFWSKH 44
DB 33 SHFEETIQGNLERECIEELCSFEAREVFEENTKNEFWAKY 75

RESULT 15
O28994
ID 028994 PRELIMINARY: PRT: 138 AA.
AC 028994;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Mature porcine factor IX (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Liver;
RC Tissue=Liver;
RA Lollar P.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U51135; AAA96318.1;
DR HSP: P00740; IEDM.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.

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DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_IT.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1 138
FT NON_TER 138
SQ SEQUENCE 138 AA: 15515 MW: 793B4BDE4D5FAFAD CRC64;

Query Match
Best Local Similarity 38.2%; Score 76; DB 6; Length 138;
Best Local Similarity 35.3%; Pred. No. 3.4e-05;
Matches 12; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

OY 11 GSIXRXICIXICDPXAXKIFZDVDDTLAFWSKH 44
DB 4 GNLERECIEELCSFEAREVFEENTKNEFWAKY 37

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Job time : 31 secs

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OM protein - protein search, using sw model

Run on: May 13, 2003, 14:03:19 : Search time 15 Seconds
(without alignments)
86.307 Million cell updates/sec

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Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/1aa/CTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	87.9	44	3	US-08-955-636-19
2	173	86.9	44	3	US-08-955-636-24
3	173	86.9	44	3	US-08-955-636-35
4	169	84.9	44	3	US-08-955-636-1
5	169	84.9	45	2	US-08-955-832-2
6	169	84.9	419	1	US-08-295-411-1
7	169	84.9	419	2	US-08-955-471-1
8	169	84.9	419	4	US-09-667-570A-3
9	169	84.9	419	5	PCR-US92-10242-1
10	169	84.9	460	2	US-08-756-506-2
11	169	84.9	460	6	US-08-756-506-4
12	169	84.9	460	6	5270178-13
13	169	84.9	460	6	5270178-14
14	169	84.9	460	6	5270178-15
15	169	84.9	460	6	5270178-16
16	169	84.9	461	6	5225537-2
17	169	84.9	461	6	5270178-17
18	169	84.9	461	6	5270178-18
19	169	84.9	461	6	5460953-3
20	167	83.9	44	3	US-08-955-636-20
21	167	83.9	44	3	US-08-955-636-21
22	167	83.9	44	3	US-08-955-636-25
23	166	83.4	44	3	US-08-955-636-22
24	156	78.4	42	2	US-08-745-254A-2
25	156	78.4	461	6	5270178-2
26	152	76.4	41	1	US-08-229-280-5
27	138	69.3	410	4	US-09-065-872-1

28	138	69.3	410	4	US-09-667-570A-1	Sequence 1, Appl
29	130	65.3	409	4	US-09-065-872-2	Sequence 2, Appl
30	130	65.3	409	4	US-09-667-570A-2	Sequence 2, Appl
31	126	63.3	44	3	US-08-955-636-23	Sequence 23, Appl
32	116	58.3	44	3	US-08-955-636-2	Sequence 2, Appl
33	112	56.3	139	1	US-08-330-978-2	Sequence 2, Appl
34	112	56.3	139	1	US-08-474-042-2	Sequence 2, Appl
35	112	56.3	139	1	US-08-484-558-2	Sequence 2, Appl
36	112	56.3	139	1	US-08-774-593-2	Sequence 2, Appl
37	112	56.3	437	1	US-08-487-037-2	Sequence 2, Appl
38	112	56.3	437	1	US-08-487-037-3	Sequence 3, Appl
39	112	56.3	488	1	US-08-487-037-1	Sequence 3, Appl
40	108	54.3	487	1	US-08-469-486-53	Sequence 53, Appl
41	108	54.3	487	2	US-08-469-658-53	Sequence 53, Appl
42	108	54.3	492	1	US-08-469-486-2	Sequence 2, Appl
43	108	54.3	492	2	US-08-469-658-2	Sequence 2, Appl
44	107	53.8	448	1	US-08-295-411-3	Sequence 3, Appl
45	107	53.8	448	2	US-08-955-471-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
US-08-955-636-19
; Sequence 19, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisseu, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)...(40)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-19

Query Match      87.9%; Score 175; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.2e-22;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ANSEFLXXLRHSGSLXRCXCIXCDFFXXAKXIFZVDDTLAFWSKH 44
Db      1 ANSEFLXXLRHSGSLXRCXCIXCDFFXXAKXIFZVDDTLAFWSKH 44

RESULT 2
US-08-955-636-24
; Sequence 24, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelisseu, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-24

Query Match 86.9%; Score 173; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 2.5e-22;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILRXICIXICDFXXAKXIFZVDVDTLAFWSKH 44
DB 1 ANSFLXLRHGSILRXICIXICDFXXAKXIFZVDVDTLAFWSKH 44

RESULT 3
US-08-955-636-35

Sequence 35, Application US/08955636A
Patent No. 6017862

GENERAL INFORMATION:

APPLICANT: Nelstuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 35

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-35

Query Match 86.9%; Score 173; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 2.5e-22;
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILRXICIXICDFXXAKXIFZVDVDTLAFWSKH 44
DB 1 ANSFLXLRHGSILRXICIXICDFXXAKXIFZVDVDTLAFWSKH 44

RESULT 4
US-08-955-636-1

Sequence 1, Application US/08955636A

Patent No. 6017862

GENERAL INFORMATION:

APPLICANT: Nelstuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 1

LENGTH: 44

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (0)...(0)

OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-08-955-636-1

Query Match 84.9%; Score 169; DB 3; Length 44;
Best Local Similarity 93.2%; Pred. No. 1.2e-21;
Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILRXICIXICDFXXAKXIFZVDVDTLAFWSKH 44
DB 1 ANSFLXLRHGSILRXICIXICDFXXAKXIFZVDVDTLAFWSKH 44

RESULT 5
US-08-965-832-2

Sequence 2, Application US/08965832

Patent No. 5847085

GENERAL INFORMATION:

APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV

TITLE OF INVENTION: Modified Protein C

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patricia L. Pabst

STREET: 2800 One Atlantic Center, 1201 West

STREET: Peachtree Street

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/965,832

FILING DATE: 7-NOV-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/745,254

FILING DATE: 8-NOV-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/053,768

FILING DATE: 25-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patricia L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRF 165/167

TELEPHONE: (404)-873-8794

TELEFAX: (404)-873-8795

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29

OTHER INFORMATION: /note="where Xaa means gamma

OTHER INFORMATION: carboxyglutamic acid"

NAME/KEY: LOCATION:

LOCATION:

OTHER INFORMATION: /note="partial sequence of human protein C"

US-08-965-832-2

Query Match 84.9%; Score 169; DB 2; Length 45;
Best Local Similarity 93.2%; Pred. No. 1.2e-21;
Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSILRXICIXICDFXXAKXIFZVDVDTLAFWSKH 44
DB 1 ANSFLXLRHGSILRXICIXICDFXXAKXIFZVDVDTLAFWSKH 44

RESULT 6
US-08-295-411-1

Sequence 1, Application US/08295411

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; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESS: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Filling, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..157
; OTHER INFORMATION: /note="Protein C Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 158..169
; OTHER INFORMATION: /note="Protein C Activation
; FEATURE:
; NAME/KEY: Region
; LOCATION: 170..419
; OTHER INFORMATION: /note="Protein C Heavy Chain"
; US-08-295-411-1
;
; Query Match 84.9%; Score 169; DB 1; Length 419;
; Best Local Similarity 72.7%; Pred. No. 1.5e-20;
; Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
;
; QY 1 ANSFLXLRHGSIXRCIXXICDPFXAKXIFZVDVDTLAFWSKH 44
; DB 1 ANSFLLELRHSSLERCIEICDFEAKEIFQVNDTLAFWSKH 44
;
; RESULT 7
; US-08-955-471-1
; Sequence 1, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
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; APPLICANT: Griffin, John H.
; APPLICANT: Masters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESS: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Filling, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..157
; OTHER INFORMATION: /note="Protein C Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 158..169
; OTHER INFORMATION: /note="Protein C Activation
; FEATURE:
; NAME/KEY: Region
; LOCATION: 170..419
; OTHER INFORMATION: /note="Protein C Heavy Chain"
; US-08-955-471-1
;
; Query Match 84.9%; Score 169; DB 2; Length 419;
; Best Local Similarity 72.7%; Pred. No. 1.5e-20;
; Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
;
; QY 1 ANSFLXLRHGSIXRCIXXICDPFXAKXIFZVDVDTLAFWSKH 44
; DB 1 ANSFLLELRHSSLERCIEICDFEAKEIFQVNDTLAFWSKH 44
;
; RESULT 8
; US-09-667-570A-3
; Sequence 3, Application US/09667570A
; Patent No. 6436397
; GENERAL INFORMATION:
; APPLICANT: Baker, Jeffrey C
; APPLICANT: Carlson, Andrew D
```

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; APPLICANT: Huang, Lihua
; APPLICANT: Sheliga, Theodore A
; TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
; FILE REFERENCE: X-11796A
; CURRENT APPLICATION NUMBER: US/09/667,570A
; CURRENT FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/045,255
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-667-570A-3

Query Match          84.9%; Score 169; DB 4; Length 419;
Best Local Similarity 72.7%; Pred. No. 1.5e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANSFLXXLRHGSIXRXCIXXICDPXXAKXIFZVDVDTLAFWSKH 44
Db 1 ANSFLRLRHSLSRECIETICDFEAKKEIFQVNDTLAFWSKH 44

RESULT 9
PCT-US92-10242-1
; Sequence 1, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Westers, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRO472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..157
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; OTHER INFORMATION: /note="Protein C Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 158..169
; OTHER INFORMATION: /note="Protein C Activation
; OTHER INFORMATION: Peptide"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 170..419
; OTHER INFORMATION: /note="Protein C Heavy Chain"
; PCT-US92-10242-1

Query Match          84.9%; Score 169; DB 5; Length 419;
Best Local Similarity 72.7%; Pred. No. 1.5e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANSFLXXLRHGSIXRXCIXXICDPXXAKXIFZVDVDTLAFWSKH 44
Db 1 ANSFLRLRHSLSRECIETICDFEAKKEIFQVNDTLAFWSKH 44

RESULT 10
US-08-756-506-2
; Sequence 2, Application US/08756506
; Patent No. 5905185
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Cottingham, Ian R.
; APPLICANT: Temperley, Simon M.
; APPLICANT: Foster, Donald C.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prunkard, Donna E.
; TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
; TITLE OF INVENTION: ANIMALS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,506
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 95-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6672
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 460 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-506-2

Query Match          84.9%; Score 169; DB 2; Length 460;
Best Local Similarity 72.7%; Pred. No. 1.7e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 ANSFLXXLRHGSIXRXCIXXICDPXXAKXIFZVDVDTLAFWSKH 44
Db 43 ANSFLRLRHSLSRECIETICDFEAKKEIFQVNDTLAFWSKH 86
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```
RESULT 11
US-08-756-506-4
: Sequence 4, Application US/08756506
: Patent No. 5905185
: GENERAL INFORMATION:
: APPLICANT: Garner, Ian
: APPLICANT: Cottingham, Ian R.
: APPLICANT: Temperley, Simon M.
: APPLICANT: Foster, Donald C.
: APPLICANT: Sprecher, Cindy A.
: APPLICANT: Brunkard, Donna E.
: TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
: TITLE OF INVENTION: ANIMALS
: NUMBER OF SEQUENCES: 25.
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ZymoGenetics, Inc.
: STREET: 1201 Eastlake Avenue East
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/756,506
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Savitskiak, Deborah A
: REGISTRATION NUMBER: 37,438
: REFERENCE/DOCKET NUMBER: 95-28
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-442-6672
: TELEFAX: 206-442-6678
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 460 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-756-506-4

Query Match      84.9%; Score 169; DB 2; Length 460;
Best Local Similarity 72.7%; Pred. No. 1.7e-20;
Matches 32: Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSGLXRCIXICDFXXAKXIFZVDVDTLAFWSKH 44
Db 43 ANSFLELRHSSLRECEIEICDFEAKEIFONVDDTLAFWSKH 86

RESULT 12
5270178-13
: Patent No. 5270178
: APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
: TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
: ZYMOGEN FORMS OF HUMAN PROTEIN C
: NUMBER OF SEQUENCES: 21
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/484,133
: FILING DATE: 23-FEB-1990
: SEQ ID NO:13:
: LENGTH: 460
: 5270178-13

Query Match      84.9%; Score 169; DB 6; Length 460;
Best Local Similarity 72.7%; Pred. No. 1.7e-20;
Matches 32: Conservative 2; Mismatches 10; Indels 0; Gaps 0;
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QY 1 ANSFLXLRHGSGLXRCIXICDFXXAKXIFZVDVDTLAFWSKH 44
Db 43 ANSFLELRHSSLRECEIEICDFEAKEIFONVDDTLAFWSKH 86

RESULT 13
5270178-14
: Patent No. 5270178
: APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
: TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
: ZYMOGEN FORMS OF HUMAN PROTEIN C
: NUMBER OF SEQUENCES: 21
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/484,133
: FILING DATE: 23-FEB-1990
: SEQ ID NO:14:
: LENGTH: 460
: 5270178-14

Query Match      84.9%; Score 169; DB 6; Length 460;
Best Local Similarity 72.7%; Pred. No. 1.7e-20;
Matches 32: Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSGLXRCIXICDFXXAKXIFZVDVDTLAFWSKH 44
Db 43 ANSFLELRHSSLRECEIEICDFEAKEIFONVDDTLAFWSKH 86

RESULT 14
5270178-15
: Patent No. 5270178
: APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
: TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
: ZYMOGEN FORMS OF HUMAN PROTEIN C
: NUMBER OF SEQUENCES: 21
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/484,133
: FILING DATE: 23-FEB-1990
: SEQ ID NO:15:
: LENGTH: 460
: 5270178-15

Query Match      84.9%; Score 169; DB 6; Length 460;
Best Local Similarity 72.7%; Pred. No. 1.7e-20;
Matches 32: Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSGLXRCIXICDFXXAKXIFZVDVDTLAFWSKH 44
Db 43 ANSFLELRHSSLRECEIEICDFEAKEIFONVDDTLAFWSKH 86

RESULT 15
5270178-16
: Patent No. 5270178
: APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
: TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
: ZYMOGEN FORMS OF HUMAN PROTEIN C
: NUMBER OF SEQUENCES: 21
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/484,133
: FILING DATE: 23-FEB-1990
: SEQ ID NO:16:
: LENGTH: 460
: 5270178-16

Query Match      84.9%; Score 169; DB 6; Length 460;
Best Local Similarity 72.7%; Pred. No. 1.7e-20;
Matches 32: Conservative 2; Mismatches 10; Indels 0; Gaps 0;
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Search completed: May 13, 2003, 14:07:23
Job time : 16 secs

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Query Match          91.0%; Score 181; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 1.6e-22;
Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0

QY 1 ANSFLXLRHGS�XRXCIXICDFFXAKXIFDQVDDTLAFWSKH 44
    ||||| ||||| || ||||| || ||||| ||||| |||||
Db 1 ANSFLLELRHGSLERECIIEICDFFEAKEIFEDVDTLAFWSKH 44

RESULT 4
US-10-182-263-6
: Sequence 6, Application US/10182263
: Publication No. US20030022354A1
: GENERAL INFORMATION:
: APPLICANT: Gerlitz, Bruce E
: APPLICANT: Jones, Bryan E
: APPLICANT: Grinnell, Brian W
: TITLE OF INVENTION: PROTEIN C DERIVATIVES
: FILE REFERENCE: X-13611
: CURRENT APPLICATION NUMBER: US/10/182,263
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: 60/181948
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-182-263-5

Query Match          91.0%; Score 181; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 1.6e-22;
Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0

QY 1 ANSFLXLRHGS�XRXCIXICDFFXAKXIFDQVDDTLAFWSKH 44
    ||||| ||||| || ||||| || ||||| ||||| |||||
Db 1 ANSFLLELRHGSLERECIIEICDFFEAKEIFEDVDTLAFWSKH 44

RESULT 3
US-10-182-263-5
: Sequence 5, Application US/10182263
: Publication No. US20030022354A1
: GENERAL INFORMATION:
: APPLICANT: Gerlitz, Bruce E
: APPLICANT: Jones, Bryan E
: APPLICANT: Grinnell, Brian W
: TITLE OF INVENTION: PROTEIN C DERIVATIVES
: FILE REFERENCE: X-13611
: CURRENT APPLICATION NUMBER: US/10/182,263
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: 60/181948
: PRIOR FILING DATE: 2002-02-11
: PRIOR APPLICATION NUMBER: 60/189199
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-182-263-4

Query Match          91.0%; Score 181; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 1.6e-22;
Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0

QY 1 ANSFLXLRHGS�XRXCIXICDFFXAKXIFDQVDDTLAFWSKH 44
    ||||| ||||| || ||||| || ||||| ||||| |||||
Db 1 ANSFLLELRHGSLERECIIEICDFFEAKEIFEDVDTLAFWSKH 44

RESULT 3
US-10-182-263-4
: Sequence 4, Application US/10182263
: Publication No. US20030022354A1
: GENERAL INFORMATION:
: APPLICANT: Gerlitz, Bruce E
: APPLICANT: Jones, Bryan E
: APPLICANT: Grinnell, Brian W
: TITLE OF INVENTION: PROTEIN C DERIVATIVES
: FILE REFERENCE: X-13611
: CURRENT APPLICATION NUMBER: US/10/182,263
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: 60/181948
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-182-263-3

Query Match          91.0%; Score 181; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 1.6e-22;
Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0

QY 1 ANSFLXLRHGS�XRXCIXICDFFXAKXIFDQVDDTLAFWSKH 44
    ||||| ||||| || ||||| || ||||| ||||| |||||
Db 1 ANSFLLELRHGSLERECIIEICDFFEAKEIFEDVDTLAFWSKH 44

RESULT 4
US-10-182-263-3
: Sequence 3, Application US/10182263
: Publication No. US20030022354A1
: GENERAL INFORMATION:
: APPLICANT: Gerlitz, Bruce E
: APPLICANT: Jones, Bryan E
: APPLICANT: Grinnell, Brian W
: TITLE OF INVENTION: PROTEIN C DERIVATIVES
: FILE REFERENCE: X-13611
: CURRENT APPLICATION NUMBER: US/10/182,263
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: 60/181948
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-182-263-2

Query Match          91.0%; Score 181; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 1.6e-22;
Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0

QY 1 ANSFLXLRHGS�XRXCIXICDFFXAKXIFDQVDDTLAFWSKH 44
    ||||| ||||| || ||||| || ||||| ||||| |||||
Db 1 ANSFLLELRHGSLERECIIEICDFFEAKEIFEDVDTLAFWSKH 44

RESULT 4
US-10-182-263-2
: Sequence 2, Application US/10182263
: Publication No. US20030022354A1
: GENERAL INFORMATION:
: APPLICANT: Gerlitz, Bruce E
: APPLICANT: Jones, Bryan E
: APPLICANT: Grinnell, Brian W
: TITLE OF INVENTION: PROTEIN C DERIVATIVES
: FILE REFERENCE: X-13611
: CURRENT APPLICATION NUMBER: US/10/182,263
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: 60/181948
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-182-263-1

Query Match          91.0%; Score 181; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 1.6e-22;
Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0

QY 1 ANSFLXLRHGS�XRXCIXICDFFXAKXIFDQVDDTLAFWSKH 44
    ||||| ||||| || ||||| || ||||| ||||| |||||
Db 1 ANSFLLELRHGSLERECIIEICDFFEAKEIFEDVDTLAFWSKH 44

RESULT 4
US-10-182-263-1
: Sequence 1, Application US/10182263
: Publication No. US20030022354A1
: GENERAL INFORMATION:
: APPLICANT: Gerlitz, Bruce E
: APPLICANT: Jones, Bryan E
: APPLICANT: Grinnell, Brian W
: TITLE OF INVENTION: PROTEIN C DERIVATIVES
: FILE REFERENCE: X-13611
: CURRENT APPLICATION NUMBER: US/10/182,263
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: 60/181948
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-182-263-0

Query Match          91.0%; Score 181; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 1.6e-22;
Matches 34; Conservative 1; Mismatches 9; Indels 0; Gaps 0

QY 1 ANSFLXLRHGS�XRXCIXICDFFXAKXIFDQVDDTLAFWSKH 44
    ||||| ||||| || ||||| || ||||| ||||| |||||
Db 1 ANSFLLELRHGSLERECIIEICDFFEAKEIFEDVDTLAFWSKH 44

RESULT 4
US-10-182-263-0
: Sequence 0, Application US/10182263
: Publication No. US20030022354A1
: GENERAL INFORMATION:
: APPLICANT: Gerlitz, Bruce E
: APPLICANT: Jones, Bryan E
: APPLICANT: Grinnell, Brian W
: TITLE OF INVENTION: PROTEIN C DERIVATIVES
: FILE REFERENCE: X-13611
: CURRENT APPLICATION NUMBER: US/10/182,263
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: 60/181948
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 0
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-182-263-0

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```

      : NUMBER OF SEQ ID NOS: 12  

      : SOFTWARE: PatentIn version 3.1  

      : SEQ ID NO 6  

        LENGTH: 419  

      TYPE: PRT  

     ORGANISM: Homo sapiens  

US-10-182-263-6
```

Query Match 86.9% Score 173; DB 9; Length 419;
Best Local Similarity .75.0%; Pred No. 3.6e-21;

Matches 33; Conservative 1; Mismatches 10; Indels 0; Gaps 0

```

OY       1 ANSFLLXLRHGS�XRXCIXICDFFXXAKKIFZDVDDTLAFWSKH   44
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 
Db        1 ANSFLFELRQCSLSRECIIEICDFEFBAKEIFCVNDDTLAFWSKH   44
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 

RESULT 5
US-10-182-263-1
: Sequence 1, Application US/10182263
: Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
PRIOR FILING DATE: 2002-07-22
PRIORITY FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln version 3.1
SEQ ID NO 1
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-1
```

Query Match 84.9% Score 169; DB 9; Length 419;
Best Local Similarity 72.7%; Pred No. 1.7e-20;

Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0

```
OY       1 ANSFLLXLRHGSLXRXCIXICDFFXXAKKIFZDVDDTLAFWSKH   44
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 
Db        1 ANSFLFELRHSSLSRECIIEICDFEFAKEIFCVNDDTLAFWSKH   44
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 

RESULT 6
US-09-978-917A-4
: Sequence 4, Application US/09978917A
: Publication No. US20030027299A1
GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 021905310 - protein C
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-917A-4
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Query Match 84.9% Score 169; DB 9; Length 419;
Best Local Similarity 72.7%; Pred No. 1.7e-20;

Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0

```
OY       1 ANSFLLXLRHGSLXRXCIXICDFFXXAKKIFZDVDDTLAFWSKH   44
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```

Db      1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 44

```

RESULT 7

US-10-182-263-2
; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
GENERAL INFORMATION

1 APPLICANT: Gruneltz, Bruce E
 2 APPLICANT: Jones, Bryan E
 3 APPLICANT: Grinnell, Brian W
 4 TITLE OF INVENTION: PROTEIN C DERIVATIVES
 5 FILE REFERENCE: X-13611
 6 CURRENT APPLICATION NUMBER: US/10/182,263
 7 CURRENT FILING DATE: 2002-07-22
 8 PRIOR APPLICATION NUMBER: 60/181948
 9 PRIOR FILING DATE: 2002-02-11
 10 PRIOR APPLICATION NUMBER: 60/189199
 11 PRIOR FILING DATE: 2000-03-14
 12 NUMBER OF SEQ. ID NOS: 12
 13 SOFTWARE: PatentIn version 3.1.1
 14 SEQ ID NO. 2

US-10-182-263-2

Query Match	84.9%	Score 169	DB 9	Length 461
Best Local Similarity	72.7%	Pred. No. 1.9e-20		
Matches 32; Conservative	2;	Mismatches 10;	Indels 0;	Gaps 0

Qy 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFZDVDDTLAFWSKH 44
||| ||| | | | | | : | | | | |
Db 43 ANSFLEELRHSSLEREIEICDFEAKEIFQNVDDTLAFWSKH 86

US-09-978-917A-2

; Sequence 2, Application US/09978917A
; Publication No. US20030027299A1

```

1  APPLICANT: Maxygen Aps; Maxygen Holdings
2  TITLE OF INVENTION: Protein C or activated protein C-like molecules
3  FILE REFERENCE: 0219u9310 - protein C
4  CURRENT APPLICATION NUMBER: US/09/978,917A
5  CURRENT FILING DATE: 2001-10-17
6  NUMBER OF SEQ ID NOS: 48
7  SOFTWARE: PatentIn Ver. 2.1

```

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; NAME/KEY: CHAIN
; LOCATION: (43)..(461)
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; FEATURE:
; LOCATION: (1)..(42)
; NAME/KEY: CHAIN
; LOCATION: (43)..(461)

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Query Match	84.9%	Score 169	DB 9	Length 461
Best Local Similarity	72.7%	Pred. No. 1.9e+20		
Matches 32: Conservative	2	Mismatches 10	Indels 0	Gaps 0

```

Oy 1 ANSFLXXLRHGS LXRCIXIXICDFXXAKXIFZDVDDTLAFWSKH 44
    |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 43 ANSFLBELRHSSLERECTEEICDFEEAKEIFQNVDDTLAFWSKH 86

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RESULT 9

US-10-109-498-1
; Sequence 1, Application US/10109498

```

; Publication NO. US20030044908A1
;
; GENERAL INFORMATION:

```

```

APPLICANT: Persson, Egon
: TITLE OF INVENTION: Coagulation Factor VII Derivatives
: FILE REFERENCE: 6286.200-US
: CURRENT APPLICATION NUMBER: US/10/109,498
: CURRENT FILING DATE: 2002-03-22
: PRIOR APPLICATION NUMBER: 60/281,261
: PRIOR FILING DATE: 2001-04-03
: PRIOR APPLICATION NUMBER: PA 2001 00477
: PRIOR FILING DATE: 2001-03-22
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 406
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (1)..(406)
: OTHER INFORMATION: Xaa = Any Amino acid
: OS-10-109-498-1

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Query Match	47.7%	Score 95:	DB 9;	Length	406;
Best Local Similarity	70.7%	Pred. No.	5.8e-08;		
Matches	29;	Conservative	3;	Mismatches	9;
				Indels	0;
				Gaps	0

```
QY      1 ANSFLXLRHGS�XRXCIXICDFFXXAKXIIFZDVDDTLAFW 41
        ||:||||| ||||| ||||| :|||: | ||
Db      1 ANAFLXLRLPGSLRXCKXXQCSPFXARXIFKDAVRTKLFW 41
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RESULT 10
US-09-759-130B-313

; Sequence 313, Application US/09759130B
; Publication No. US20030022279A1

APPLICANT: Millennium Pharmaceuticals, Inc

```

; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 313
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-313

Query Match
Best Local Similarity 41.2%; Score 84; DB 9; Length 96;
Matches 14; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 11 GSLRXXCIXXICDFXXKXIFZDVDDTLAFWSKH 44
DB 46 GNLRECNELCNVEARELFVDEDKTIAFWQXY 79

RESULT 11
US-10-189-123-43
; Sequence 43, Application US/10189123
; Publication No. US20030082586A1
; GENERAL INFORMATION:
; APPLICANT: KIRST, Susan J.
; APPLICANT: HOLTZMAN, Douglas A.
; APPLICANT: FRASER, Christopher C.
; APPLICANT: SHARP, John D.
; APPLICANT: BARNES, Thomas S.
; TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: 10147-1103
; CURRENT APPLICATION NUMBER: US/10/189,123
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/342,364
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 43
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-123-43

Query Match
Best Local Similarity 42.2%; Score 84; DB 9; Length 96;
Matches 14; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 11 GSLRXXCIXXICDFXXKXIFZDVDDTLAFWSKH 44
DB 46 GNLRECNELCNVEARELFVDEDKTIAFWQXY 79

RESULT 12
US-09-759-130B-312
; Sequence 312, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Sharp, John D.
; APPLICANT: Barnes, Thomas S.
; APPLICANT: Kirst, Susan J.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Myers, Paul S.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodheart, Andrew
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
```

```

; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 312
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-312

Query Match
Best Local Similarity 42.2%; Score 84; DB 9; Length 209;
Matches 14; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 11 GSLRXXCIXXICDFXXKXIFZDVDDTLAFWSKH 44
DB 46 GNLRECNELCNVEARELFVDEDKTIAFWQXY 79

RESULT 13
US-10-189-123-42
; Sequence 42, Application US/10189123
; Publication No. US20030082586A1
; GENERAL INFORMATION:
; APPLICANT: KIRST, Susan J.
; APPLICANT: HOLTZMAN, Douglas A.
; APPLICANT: FRASER, Christopher C.
; APPLICANT: SHARP, John D.
; APPLICANT: BARNES, Thomas S.
; TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: 10147-1103
; CURRENT APPLICATION NUMBER: US/10/189,123
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 42
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-123-42

Query Match
Best Local Similarity 42.2%; Score 84; DB 9; Length 209;
Matches 14; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 11 GSLRXXCIXXICDFXXKXIFZDVDDTLAFWSKH 44
```


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